



811252

SEQUENCE LISTING

<110> The Government of the United States of America, as
represented by the Secretary of the Department of Health and
Human Services, Centers for Disease Control and Prevention
Chang, Gwong-Jen J.

<120> NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION

<130> 6395-64909-02

<140> 10/500,796
<141> 2004-07-06

<150> PCT/US02/10764
<151> 2002-04-04

<150> 09/826,115
<151> 2001-04-04

<150> 09/701,536
<151> 2000-11-29

<150> PCT/US99/12298
<151> 1999-06-03

<150> 60/087,908
<151> 1998-06-04

<160> 64

<170> PatentIn version 3.3

<210> 1
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<222> (1)..(48)
<223> Amplimer 14DV389

<220>
<221> CDS
<222> (25)..(48)

<400> 1
cttggtacct ctagagccgc cgcc atg ggc aga aag caa aac aaa aga 48
Met Gly Arg Lys Gln Asn Lys Arg
1 5

<210> 2
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

811252

<223> Synthetic Construct

<400> 2

Met Gly Arg Lys Gln Asn Lys Arg
1 5

<210> 3

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> misc_feature

<222> (1)..(50)

<223> Amplimer c14DV2453

<400> 3

ttttcttttg cgcccgctca aacttaagca tgcacattgg tcgctaagaa 50

<210> 4

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> misc_feature

<222> (1)..(48)

<223> Amplimer YFDV389

<220>

<221> CDS

<222> (25)..(48)

<400> 4

cttggtacct ctagagccgc cgcc atg cgt tcc cat gat gtt ctg act 48
Met Arg Ser His Asp Val Leu Thr
1 5

<210> 5

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 5

Met Arg Ser His Asp Val Leu Thr
1 5

811252

<210> 6
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<222> (1)..(41)
<223> Amplimer cYFDV2452

<400> 6
ttttcttttg cggccgctca cgccccaact cctagagaaa c 41

<210> 7
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<222> (1)..(51)
<223> Amplimer SLEDV410

<220>
<221> CDS
<222> (25)..(51)
<400> 7
cttggtacct ctagagccgc cgcc atg tct aaa aaa aga gga ggg acc aga 51
Met Ser Lys Lys Arg Gly Gly Thr Arg
1 5

<210> 8
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 8
Met Ser Lys Lys Arg Gly Gly Thr Arg
1 5

<210> 9
<211> 38
<212> DNA
<213> Artificial Sequence

<220>

811252

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> misc_feature

<222> (1)..(38)

<223> Amplimer CSLEDV2449

<400> 9

ttttcttttg cggccgctta ggcttgacg ctggttgc

38

<210> 10

<211> 7500

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> misc_feature

<222> (1)..(7500)

<223> pCDJE 2-7

<220>

<221> CDS

<222> (916)..(3009)

<400> 10

gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg 60

ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120

cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180

ttagggtag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240

gattattgac tagttattaa tagtaataaa ttacgggggtc attagttcat agcccatata 300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360

cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420

attgacgtca atgggtggac tatttacggt aaactgccc cttggcagta catcaagtgt 480

atcatatgcc aagtagcccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540

atgccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca 600

tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 660

actcacgggg atttccaagt ctccaccca ttgacgtcaa tgggagtttg ttttggcacc 720

aaaatcaacg ggactttcca aaatgtcgta acaactccgc ccattgacg caaatgggcg 780

gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaacca 840

ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttggtacc 900

gagctcgccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa 951

Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu

811252																
1				5				10								
ggc	tca	atc	atg	tgg	ctc	gcg	agc	ttg	gca	gtt	gtc	ata	gct	tgt	gcg	999
Gly	Ser	Ile	Met	Trp	Leu	Ala	Ser	Leu	Ala	Val	Val	Ile	Ala	Cys	Ala	
		15					20					25				
gga	gcc	atg	aag	ttg	tcg	aat	ttc	cag	ggg	aag	ctt	ttg	atg	acc	atc	1047
Gly	Ala	Met	Lys	Leu	Ser	Asn	Phe	Gln	Gly	Lys	Leu	Leu	Met	Thr	Ile	
	30					35					40					
aac	aac	acg	gac	att	gca	gac	gtt	atc	gtg	att	ccc	acc	tca	aaa	gga	1095
Asn	Asn	Thr	Asp	Ile	Ala	Asp	Val	Ile	Val	Ile	Pro	Thr	Ser	Lys	Gly	
45					50					55					60	
gag	aac	aga	tgc	tgg	gtc	cgg	gca	atc	gac	gtc	ggc	tac	atg	tgt	gag	1143
Glu	Asn	Arg	Cys	Trp	Val	Arg	Ala	Ile	Asp	Val	Gly	Tyr	Met	Cys	Glu	
			65						70					75		
gac	act	atc	acg	tac	gaa	tgt	cct	aag	ctt	acc	atg	ggc	aat	gat	cca	1191
Asp	Thr	Ile	Thr	Tyr	Glu	Cys	Pro	Lys	Leu	Thr	Met	Gly	Asn	Asp	Pro	
			80					85					90			
gag	gat	gtg	gat	tgc	tgg	tgt	gac	aac	caa	gaa	gtc	tac	gtc	caa	tat	1239
Glu	Asp	Val	Asp	Cys	Trp	Cys	Asp	Asn	Gln	Glu	Val	Tyr	Val	Gln	Tyr	
		95					100					105				
gga	cgg	tgc	acg	cgg	acc	agg	cat	tcc	aag	cga	agc	agg	aga	tcc	gtg	1287
Gly	Arg	Cys	Thr	Arg	Thr	Arg	His	Ser	Lys	Arg	Ser	Arg	Arg	Ser	Val	
	110					115					120					
tcg	gtc	caa	aca	cat	ggg	gag	agt	tca	cta	gtg	aat	aaa	aaa	gag	gct	1335
Ser	Val	Gln	Thr	His	Gly	Glu	Ser	Ser	Leu	Val	Asn	Lys	Lys	Glu	Ala	
125					130					135					140	
tgg	ctg	gat	tca	acg	aaa	gcc	aca	cga	tat	ctc	atg	aaa	act	gag	aac	1383
Trp	Leu	Asp	Ser	Thr	Lys	Ala	Thr	Arg	Tyr	Leu	Met	Lys	Thr	Glu	Asn	
			145						150					155		
tgg	atc	ata	agg	aat	cct	ggc	tat	gct	ttc	ctg	gcg	gcg	gta	ctt	ggc	1431
Trp	Ile	Ile	Arg	Asn	Pro	Gly	Tyr	Ala	Phe	Leu	Ala	Ala	Val	Leu	Gly	
			160					165					170			
tgg	atg	ctt	ggc	agt	aac	aac	ggt	caa	cgc	gtg	gta	ttt	acc	atc	ctc	1479
Trp	Met	Leu	Gly	Ser	Asn	Asn	Gly	Gln	Arg	Val	Val	Phe	Thr	Ile	Leu	
		175					180					185				
ctg	ctg	ttg	gtc	gct	ccg	gct	tac	agt	ttt	aat	tgt	ctg	gga	atg	ggc	1527
Leu	Leu	Leu	Val	Ala	Pro	Ala	Tyr	Ser	Phe	Asn	Cys	Leu	Gly	Met	Gly	
	190					195					200					
aat	cgt	gac	ttc	ata	gaa	gga	gcc	agt	gga	gcc	act	tgg	gtg	gac	ttg	1575
Asn	Arg	Asp	Phe	Ile	Glu	Gly	Ala	Ser	Gly	Ala	Thr	Trp	Val	Asp	Leu	
205					210					215					220	
gtg	ctg	gaa	gga	gat	agc	tgc	ttg	aca	atc	atg	gca	aac	gac	aaa	cca	1623
Val	Leu	Glu	Gly	Asp	Ser	Cys	Leu	Thr	Ile	Met	Ala	Asn	Asp	Lys	Pro	
				225					230					235		
aca	ttg	gac	gtc	cgc	atg	att	aac	atc	gaa	gct	agc	caa	ctt	gct	gag	1671
Thr	Leu	Asp	Val	Arg	Met	Ile	Asn	Ile	Glu	Ala	Ser	Gln	Leu	Ala	Glu	
			240					245					250			
gtc	aga	agt	tac	tgc	tat	cat	gct	tca	gtc	act	gac	atc	tcg	acg	gtg	1719

Val	Arg	Ser	Tyr	Cys	Tyr	His	Ala	Ser	Val	Thr	Asp	Ile	Ser	Thr	Val	
		255					260					265				
gct	cgg	tgc	ccc	acg	act	gga	gaa	gcc	cac	aac	gag	aag	cga	gct	gat	1767
Ala	Arg	Cys	Pro	Thr	Thr	Gly	Glu	Ala	His	Asn	Glu	Lys	Arg	Ala	Asp	
	270					275					280					
agt	agc	tat	gtg	tgc	aaa	caa	ggc	ttc	act	gac	cgt	ggg	tgg	ggc	aac	1815
Ser	Ser	Tyr	Val	Cys	Lys	Gln	Gly	Phe	Thr	Asp	Arg	Gly	Trp	Gly	Asn	
285					290					295					300	
gga	tgt	gga	ctt	ttc	ggg	aag	gga	agc	att	gac	aca	tgt	gca	aaa	ttc	1863
Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile	Asp	Thr	Cys	Ala	Lys	Phe	
				305					310					315		
tcc	tgc	acc	agt	aaa	gcg	att	ggg	aga	aca	atc	cag	cca	gaa	aac	atc	1911
Ser	Cys	Thr	Ser	Lys	Ala	Ile	Gly	Arg	Thr	Ile	Gln	Pro	Glu	Asn	Ile	
			320					325					330			
aaa	tac	gaa	gtt	ggc	att	ttt	gtg	cat	gga	acc	acc	act	tcg	gaa	aac	1959
Lys	Tyr	Glu	Val	Gly	Ile	Phe	Val	His	Gly	Thr	Thr	Thr	Ser	Glu	Asn	
		335					340					345				
cat	ggg	aat	tat	tca	gcg	caa	gtt	ggg	gcg	tcc	cag	gcg	gca	aag	ttt	2007
His	Gly	Asn	Tyr	Ser	Ala	Gln	Val	Gly	Ala	Ser	Gln	Ala	Ala	Lys	Phe	
	350					355					360					
aca	gta	aca	ccc	aat	gct	cct	tcg	ata	acc	ctc	aaa	ctt	ggt	gac	tac	2055
Thr	Val	Thr	Pro	Asn	Ala	Pro	Ser	Ile	Thr	Leu	Lys	Leu	Gly	Asp	Tyr	
365					370					375					380	
gga	gaa	gtc	aca	ctg	gac	tgt	gag	cca	agg	agt	gga	ctg	aac	act	gaa	2103
Gly	Glu	Val	Thr	Leu	Asp	Cys	Glu	Pro	Arg	Ser	Gly	Leu	Asn	Thr	Glu	
				385					390					395		
gcg	ttt	tac	gtc	atg	acc	gtg	ggg	tca	aag	tca	ttt	ctg	gtc	cat	agg	2151
Ala	Phe	Tyr	Val	Met	Thr	Val	Gly	Ser	Lys	Ser	Phe	Leu	Val	His	Arg	
			400					405					410			
gag	tgg	ttt	cat	gac	ctc	gct	ctc	ccc	tgg	acg	tcc	cct	tcg	agc	aca	2199
Glu	Trp	Phe	His	Asp	Leu	Ala	Leu	Pro	Trp	Thr	Ser	Pro	Ser	Ser	Thr	
		415					420					425				
gcg	tgg	aga	aac	aga	gaa	ctc	ctc	atg	gaa	ttt	gaa	gag	gcg	cac	gcc	2247
Ala	Trp	Arg	Asn	Arg	Glu	Leu	Leu	Met	Glu	Phe	Glu	Glu	Ala	His	Ala	
	430				435						440					
aca	aaa	cag	tcc	gtt	gtt	gct	ctt	ggg	tca	cag	gaa	gga	ggc	ctc	cat	2295
Thr	Lys	Gln	Ser	Val	Val	Ala	Leu	Gly	Ser	Gln	Glu	Gly	Gly	Leu	His	
445					450					455					460	
cag	gcg	ttg	gca	gga	gcc	atc	gtg	gtg	gag	tac	tca	agc	tca	gtg	aag	2343
Gln	Ala	Leu	Ala	Gly	Ala	Ile	Val	Val	Glu	Tyr	Ser	Ser	Ser	Val	Lys	
				465					470					475		
tta	aca	tca	ggc	cac	ctg	aaa	tgt	agg	ctg	aaa	atg	gac	aaa	ctg	gct	2391
Leu	Thr	Ser	Gly	His	Leu	Lys	Cys	Arg	Leu	Lys	Met	Asp	Lys	Leu	Ala	
			480					485					490			
ctg	aaa	ggc	aca	acc	tat	ggc	atg	tgt	aca	gaa	aaa	ttc	tcg	ttc	gcg	2439
Leu	Lys	Gly	Thr	Thr	Tyr	Gly	Met	Cys	Thr	Glu	Lys	Phe	Ser	Phe	Ala	
		495					500					505				

															811252	
aaa	aat	ccg	gcg	gac	act	ggt	cac	gga	aca	gtt	gtc	att	gaa	ctc	tcc	2487
Lys	Asn	Pro	Ala	Asp	Thr	Gly	His	Gly	Thr	Val	Val	Ile	Glu	Leu	Ser	
	510					515					520					
tac	tct	ggg	agt	gat	ggc	ccc	tgc	aaa	att	ccg	att	gct	tcc	ggt	gcg	2535
Tyr	Ser	Gly	Ser	Asp	Gly	Pro	Cys	Lys	Ile	Pro	Ile	Ala	Ser	Val	Ala	
525					530					535					540	
agc	ctc	aat	gac	atg	acc	ccc	gtt	ggg	cgg	ctg	gtg	aca	gtg	aac	ccc	2583
Ser	Leu	Asn	Asp	Met	Thr	Pro	Val	Gly	Arg	Leu	Val	Thr	Val	Asn	Pro	
				545					550					555		
ttc	gtc	gcg	act	tcc	agt	gcc	agc	tca	aag	gtg	ctg	gtc	gag	atg	gaa	2631
Phe	Val	Ala	Thr	Ser	Ser	Ala	Ser	Ser	Lys	Val	Leu	Val	Glu	Met	Glu	
			560					565					570			
ccc	ccc	ttc	gga	gac	tcc	tac	atc	gta	gtt	gga	agg	gga	gac	aag	cag	2679
Pro	Pro	Phe	Gly	Asp	Ser	Tyr	Ile	Val	Val	Gly	Arg	Gly	Asp	Lys	Gln	
		575					580					585				
atc	aac	cac	cat	tgg	cac	aaa	gct	gga	agc	acg	ctg	ggc	aag	gcc	ttt	2727
Ile	Asn	His	His	Trp	His	Lys	Ala	Gly	Ser	Thr	Leu	Gly	Lys	Ala	Phe	
	590					595					600					
tca	aca	act	ttg	aag	gga	gct	caa	aga	ctg	gca	gcg	ttg	ggc	gac	aca	2775
Ser	Thr	Thr	Leu	Lys	Gly	Ala	Gln	Arg	Leu	Ala	Ala	Leu	Gly	Asp	Thr	
605					610					615					620	
gcc	tgg	gac	ttt	ggc	tct	att	gga	ggg	gtc	ttc	aac	tcc	ata	gga	aaa	2823
Ala	Trp	Asp	Phe	Gly	Ser	Ile	Gly	Gly	Val	Phe	Asn	Ser	Ile	Gly	Lys	
			625						630					635		
gcc	gtt	cac	caa	gtg	ttt	ggt	ggt	gcc	ttc	aga	aca	ctc	ttt	ggg	gga	2871
Ala	Val	His	Gln	Val	Phe	Gly	Gly	Ala	Phe	Arg	Thr	Leu	Phe	Gly	Gly	
			640					645					650			
atg	tct	tgg	atc	aca	caa	ggg	cta	atg	ggt	gcc	cta	ctg	ctc	tgg	atg	2919
Met	Ser	Trp	Ile	Thr	Gln	Gly	Leu	Met	Gly	Ala	Leu	Leu	Leu	Trp	Met	
		655					660					665				
ggc	gtc	aac	gca	cga	gac	cga	tca	att	gct	ttg	gcc	ttc	tta	gcc	aca	2967
Gly	Val	Asn	Ala	Arg	Asp	Arg	Ser	Ile	Ala	Leu	Ala	Phe	Leu	Ala	Thr	
	670					675					680					
ggg	ggt	gtg	ctc	gtg	ttc	tta	gcg	acc	aat	gtg	cat	gct	taa			3009
Gly	Gly	Val	Leu	Val	Phe	Leu	Ala	Thr	Asn	Val	His	Ala				
685					690					695						
ttagttttgag cggtccgctcg agcatgcatc tagagggcc tttctatag tgtcacctaa															3069	
atgctagagc tcgctgatca gcctcgactg tgccttctag ttgccagcca tctgttgttt															3129	
gccccctccc cgtgccttcc ttgacctgag aagggtgccac tcccactgtc ctttctaat															3189	
aaaatgagga aattgcatcg cattgtctga gtaggtgtca ttctattctg ggggggtgggg															3249	
tggggcagga cagcaagggg gaggattggg aagacaatag caggcatgct ggggatgcgg															3309	
tgggctctat ggcttctgag gcgaaagaa ccagctgggg ctctaggggg tatccccacg															3369	
cgccctgtag cggcgatta agcgcggcgg gtgtggtggt tacgcgcagc gtgaccgcta															3429	
cacttgccag cgccctagcg cccgctcctt tcgctttctt cccttccttt ctcgccacgt															3489	

811252

tcgccggctt	tccccgtcaa	gctctaaatc	ggggcatccc	tttagggttc	cgatttagtg	3549
ctttacggca	cctcgacccc	aaaaaacttg	attaggggtga	tggttcacgt	agtgggcat	3609
cgccctgata	gacgggtttt	cgccctttga	cgttggagtc	cacgttcttt	aatagtggac	3669
tcttgttcca	aactggaaca	acactcaacc	ctatctcgg	ctattctttt	gatttataag	3729
ggattttggg	gatttcggcc	tattggttaa	aaaatgagct	gatttaacaa	aaatttaacg	3789
cgaattaatt	ctgtggaatg	tgtgtcagtt	aggggtgtgga	aagtccccag	gctccccagg	3849
caggcagaag	tatgcaaagc	atgcatctca	attagtcagc	aaccagggtgt	ggaaagtccc	3909
caggctcccc	agcaggcaga	agtatgcaaa	gcatgcatct	caattagtca	gcaaccatag	3969
tcccgcccct	aactccgccc	atcccgcccc	taactccgcc	cagttccgcc	cattctccgc	4029
cccatggctg	actaattttt	tttatttatg	cagaggccga	ggccgcctct	gcctctgagc	4089
tattccagaa	gtagtgagga	ggcttttttg	gaggcctagg	cttttgcaaa	aagctcccgg	4149
gagcttgat	atccattttc	ggatctgac	aagagacagg	atgaggatcg	tttcgcatga	4209
ttgaacaaga	tggattgcac	gcaggttctc	cggccgcttg	ggtggagagg	ctattcggct	4269
atgactgggc	acaacagaca	atcggtgct	ctgatgccgc	cgtgttccgg	ctgtcagcgc	4329
agggcgccc	ggttcttttt	gtcaagaccg	acctgtccgg	tgccctgaat	gaactgcagg	4389
acgaggcagc	gcggctatcg	tggctggcca	cgacgggcgt	tccttgcgca	gctgtgctcg	4449
acgttgtcac	tgaagcggga	agggactggc	tgctattggg	cgaagtgccg	gggcaggatc	4509
tcctgtcatc	tcaccttgct	cctgccgaga	aagtatccat	catggctgat	gcaatgcggc	4569
ggctgcatac	gcttgatccg	gctacctgcc	cattcgacca	ccaagcgaaa	catcgcatcg	4629
agcagcacg	tactcggatg	gaagccggtc	ttgtcgatca	ggatgatctg	gacgaagagc	4689
atcaggggct	cgcgccagcc	gaactgttcg	ccaggctcaa	ggcgcgcatg	cccgcggcg	4749
aggatctcgt	cgtgacccat	ggcgtgcct	gcttgccgaa	tatcatgggtg	gaaaatggcc	4809
gcttttctgg	attcatcgac	tgtggccggc	tgggtgtggc	ggaccgctat	caggacatag	4869
cgttggctac	ccgtgatatt	gctgaagagc	ttggcggcga	atgggctgac	cgcttcctcg	4929
tgctttacgg	tatcgccgct	cccgattcgc	agcgcacgc	cttctatcgc	cttcttgacg	4989
agttcttctg	agcgggactc	tggggttcga	aatgaccgac	caagcgacgc	ccaacctgcc	5049
atcacgagat	ttcgattcca	ccgccgcctt	ctatgaaagg	ttgggcttcg	gaatcgtttt	5109
ccgggacgcc	ggctggatga	tcctccagcg	cggggatctc	atgctggagt	tcttcgccc	5169
ccccaaactg	tttattgcag	cttataatgg	ttacaaataa	agcaatagca	tcacaaattt	5229
cacaaataaa	gcattttttt	cactgcattc	tagttgtggt	ttgtccaaac	tcatcaatgt	5289
atcttatcat	gtctgtatac	cgtcgacctc	tagctagagc	ttggcgtaat	catggtcata	5349

811252

gctgtttcct	gtgtgaaatt	gttatccgct	cacaattcca	cacaacatac	gagccggaag	5409
cataaagtgt	aaagcctggg	gtgcctaattg	agtgagctaa	ctcacattaa	ttgcgttgcg	5469
ctcactgccc	gctttccagt	cgaggaaacct	gtcgtgccag	ctgcattaat	gaatcggcca	5529
acgcgcgggg	agaggcggtt	tgcgtatttg	gcgctcttcc	gcttcctcgc	tactgactc	5589
gctgcgctcg	gtcgttcggc	tgcggcgagc	ggtatcagct	cactcaaagg	cggtaatagc	5649
gttatccaca	gaatcagggg	ataacgcagg	aaagaacatg	tgagcaaaag	gccagcaaaa	5709
ggccaggaac	cgtaaaaagg	ccgcgttgct	ggcgtttttc	cataggctcc	gccccctga	5769
cgagcatcac	aaaaatcgac	gctcaagtca	gagggtggcg	aacccgacag	gactataaag	5829
ataccaggcg	tttccccctg	gaagctccct	cgctgcgtct	cctgttccga	ccctgccgct	5889
taccggatac	ctgtccgcct	ttctcccttc	gggaagcggt	gcgctttctc	aatgctcacg	5949
ctgtaggtat	ctcagttcgg	tgtaggtcgt	tcgctccaag	ctgggctgtg	tgcacgaacc	6009
ccccgttcag	cccgaaccgt	gcgccttatc	cggtaaactat	cgtcttgagt	ccaacccggt	6069
aagacacgac	ttatcgccac	tggcagcagc	cactggtaac	aggattagca	gagcgaggta	6129
tgtaggcggt	gctacagagt	tcttgaagtg	gtggcctaac	tacggctaca	ctagaaggac	6189
agtatttggg	atctgcgctc	tgtgaagcc	agttaccttc	ggaaaaagag	ttggtagctc	6249
ttgatccggc	aaacaaacca	ccgctggtag	cggtggtttt	tttgtttgca	agcagcagat	6309
tacgcgcaga	aaaaaaggat	ctcaagaaga	tcctttgatc	ttttctacgg	ggtctgacgc	6369
tcagtgaac	gaaaactcac	gttaagggat	tttggtcattg	agattatcaa	aaaggatctt	6429
cacctagatc	cttttaaat	aaaaatgaag	ttttaaatca	atctaaagta	tatatgagta	6489
aacttggctc	gacagttacc	aatgcttaat	cagtgaaggca	cctatctcag	cgatctgtct	6549
atttcgttca	tccatagttg	cctgactccc	cgctcgtgtg	ataactacga	tacgggaggg	6609
cttaccatct	ggccccagtg	ctgcaatgat	accgcgagac	ccacgctcac	cggctccaga	6669
tttatcagca	ataaaccagc	cagccggaag	ggccgagcgc	agaagtgggtc	ctgcaacttt	6729
atccgcctcc	atccagtcta	ttaattgttg	ccgggaagct	agagtaagta	gttcgccagt	6789
taatagtttg	cgcaacgttg	ttgccattgc	tacaggcatc	gtgggtgtcac	gctcgtcggt	6849
tggtatggct	tcattcagct	ccggttccca	acgatcaagg	cgagttacat	gatcccccat	6909
gttgtgcaaa	aaagcgggta	gttccttcgg	tcctccgatac	gttgtcagaa	gtaagttggc	6969
cgcagtgtta	tactcatg	ttatggcagc	actgcataat	tctcttactg	tcatgccatc	7029
cgtaagatgc	ttttctgtga	ctgggtgagta	ctcaaccaag	tcattctgag	aatagtgat	7089
gcggcgaccg	agttgctctt	gcccggcgctc	aatacgggat	aataccgcgc	cacatagcag	7149
aactttaaaa	gtgctcatca	ttggaaaacg	ttcttcgggg	cgaaaactct	caaggatctt	7209
accgctgttg	agatccagtt	cgatgtaacc	cactcgtgca	cccaactgat	cttcagcatc	7269

811252

ttttactttc accagcgttt ctgggtgagc aaaaacagga aggcaaatg ccgcaaaaaa 7329
 gggaataagg gcgacacgga aatgttgaat actcatactc ttcctttttc aatattattg 7389
 aagcatttat cagggttatt gtctcatgag cggatacata tttgaatgta tttagaaaaa 7449
 taaacaaata ggggttccgc gcacatttcc ccgaaaagtg ccacctgacg t 7500

<210> 11
 <211> 697
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 11

Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met
 1 5 10 15

Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys
 20 25 30

Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp
 35 40 45

Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys
 50 55 60

Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr
 65 70 75 80

Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp
 85 90 95

Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr
 100 105 110

Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr
 115 120 125

His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser
 130 135 140

Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg
 145 150 155 160

Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly
 165 170 175

811252

Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Leu Val
180 185 190

Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe
195 200 205

Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly
210 215 220

Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val
225 230 235 240

Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr
245 250 255

Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro
260 265 270

Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val
275 280 285

Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
290 295 300

Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser
305 310 315 320

Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val
325 330 335

Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr
340 345 350

Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro
355 360 365

Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr
370 375 380

Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val
385 390 395 400

Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His
405 410 415

Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn
420 425 430

811252

Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser
435 440 445

Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala
450 455 460

Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly
465 470 475 480

His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr
485 490 495

Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala
500 505 510

Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser
515 520 525

Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp
530 535 540

Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr
545 550 555 560

Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly
565 570 575

Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His
580 585 590

Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu
595 600 605

Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe
610 615 620

Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln
625 630 635 640

Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile
645 650 655

Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala
660 665 670

Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu
Page 12

675

680

811252

685

Val Phe Leu Ala Thr Asn Val His Ala
 690 695

<210> 12
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct

<220>
 <221> misc_feature
 <222> (1)..(46)
 <223> WN 466

<400> 12
 cttggtaccc gtctcggcgc cgtgaccctc tcgaacttcc agggca 46

<210> 13
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct

<220>
 <221> misc_feature
 <222> (1)..(43)
 <223> CWN2444

<400> 13
 agaggcactt gcacgtgcgg acttccgccg gcgaaaaaga aaa 43

<210> 14
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct

<220>
 <221> MISC_FEATURE
 <223> JE Signal

<400> 14

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
 1 5 10 15

Val Val Ile Ala Cys Ala Gly Ala

<210> 15
 <211> 5308
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct

<220>
 <221> misc_feature
 <222> (1)..(5308)
 <223> pCBWN

<220>
 <221> CDS
 <222> (911)..(2986)

```

<400> 15
gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctgatg      60
ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg      120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180
ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagtccat agcccatata      300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc      360
ccgccccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420
attgacgtca atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt      480
atcatatgcc aagtacgccc cttattgacg tcaatgacgg taaatggccc gcctggcatt      540
atgcccagta catgacctta tgggactttc ctacttgga gtacatctac gtattagtca      600
tcgctattac catggtgatg cggtttttgg cagtacatca atgggcgtgg atagcggttt      660
gactcacggg gatttccaag tctccacccc attgacgtca atgggagttt gttttggcac      720
caaatcaaac gggactttcc aaatgtcgt aacaactccg cccattgac gcaaatgggc      780
ggtaggcgtg tacgggtgga ggtctatata agcagagctc tctggctaac tagagaaccc      840
actgcttact ggcttatcga aattaatacg actcactata gggagacca agcttggtac      900
cgccgcccgc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg      949
          Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala
          1              5              10

agc ttg gca gtt gtc ata gct tgt gca ggc gcc gtg acc ctc tcg aac      997
Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn
  15              20              25

ttc cag ggc aag gtg atg atg acg gta aat gct act gac gtc aca gat      1045
Phe Gln Gly Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp
  30              35              40              45

```

811252

gtc atc acg att cca aca gct gct gga aag aac cta tgc att gtc aga	1093
Val Ile Thr Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg	
	50
gca atg gat gtg gga tac atg tgc gat gat act atc act tat gaa tgc	1141
Ala Met Asp Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys	
	65
cca gtg ctg tcg gct ggt aat gat cca gaa gac atc gac tgt tgg tgc	1189
Pro Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys	
	80
aca aag tca gca gtc tac gtc agg tat gga aga tgc acc aag aca cgc	1237
Thr Lys Ser Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg	
	95
cac tca aga cgc agt cgg agg tca ctg aca gtg cag aca cac gga gaa	1285
His Ser Arg Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu	
	110
	115
	120
	125
agc act cta gcg aac aag aag ggg gct tgg atg gac agc acc aag gcc	1333
Ser Thr Leu Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala	
	130
	135
aca agg tat ttg gta aaa aca gaa tca tgg atc ttg agg aac cct gga	1381
Thr Arg Tyr Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly	
	145
	150
	155
tat gcc ctg gtg gca gcc gtc att ggt tgg atg ctt ggg agc aac acc	1429
Tyr Ala Leu Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr	
	160
	165
	170
atg cag aga gtt gtg ttt gtc gtg cta ttg ctt ttg gtg gcc cca gct	1477
Met Gln Arg Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala	
	175
	180
	185
tac agc ttc aac tgc ctt gga atg agc aac aga gac ttc ttg gaa gga	1525
Tyr Ser Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly	
	190
	195
	200
	205
gtg tct gga gca aca tgg gtg gat ttg gtt ctc gaa ggc gac agc tgc	1573
Val Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys	
	210
	215
	220
gtg act atc atg tct aag gac aag cct acc atc gat gtg aag atg atg	1621
Val Thr Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met	
	225
	230
	235
aat atg gag gcg gcc aac ctg gca gag gtc cgc agt tat tgc tat ttg	1669
Asn Met Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu	
	240
	245
	250
gct acc gtc agc gat ctc tcc acc aaa gct gcg tgc ccg acc atg gga	1717
Ala Thr Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly	
	255
	260
	265
gaa gct cac aat gac aaa cgt gct gac cca gct ttt gtg tgc aga caa	1765
Glu Ala His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln	
	270
	275
	280
	285
gga gtg gtg gac agg ggc tgg ggc aac ggc tgc gga cta ttt ggc aaa	1813
Gly Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys	

														811252																											
290														295														300													
gga	agc	att	gac	aca	tgc	gcc	aaa	ttt	gcc	tgc	tct	acc	aag	gca	ata	1861																									
Gly	Ser	Ile	Asp	Thr	Cys	Ala	Lys	Phe	Ala	Cys	Ser	Thr	Lys	Ala	Ile																										
														310																											
gga	aga	acc	atc	ttg	aaa	gag	aat	atc	aag	tac	gaa	gtg	gcc	att	ttt	1909																									
Gly	Arg	Thr	Ile	Leu	Lys	Glu	Asn	Ile	Lys	Tyr	Glu	Val	Ala	Ile	Phe																										
														325																											
gtc	cat	gga	cca	act	act	gtg	gag	tcg	cac	gga	aac	tac	tcc	aca	cag	1957																									
Val	His	Gly	Pro	Thr	Thr	Val	Glu	Ser	His	Gly	Asn	Tyr	Ser	Thr	Gln																										
														340																											
gtt	gga	gcc	act	cag	gca	ggg	aga	ttc	agc	atc	act	cct	gcg	gcg	cct	2005																									
Val	Gly	Ala	Thr	Gln	Ala	Gly	Arg	Phe	Ser	Ile	Thr	Pro	Ala	Ala	Pro																										
														350																											
tca	tac	aca	cta	aag	ctt	gga	gaa	tat	gga	gag	gtg	aca	gtg	gac	tgt	2053																									
Ser	Tyr	Thr	Leu	Lys	Leu	Gly	Glu	Tyr	Gly	Glu	Val	Thr	Val	Asp	Cys																										
														370																											
gaa	cca	cgg	tca	ggg	att	gac	acc	aat	gca	tac	tac	gtg	atg	act	gtt	2101																									
Glu	Pro	Arg	Ser	Gly	Ile	Asp	Thr	Asn	Ala	Tyr	Tyr	Val	Met	Thr	Val																										
														385																											
gga	aca	aag	acg	ttc	ttg	gtc	cat	cgt	gag	tgg	ttc	atg	gac	ctc	aac	2149																									
Gly	Thr	Lys	Thr	Phe	Leu	Val	His	Arg	Glu	Trp	Phe	Met	Asp	Leu	Asn																										
														400																											
ctc	cct	tgg	agc	agt	gct	gga	agt	act	gtg	tgg	agg	aac	aga	gag	acg	2197																									
Leu	Pro	Trp	Ser	Ser	Ala	Gly	Ser	Thr	Val	Trp	Arg	Asn	Arg	Glu	Thr																										
														415																											
tta	atg	gag	ttt	gag	gaa	cca	cac	gcc	acg	aag	cag	tct	gtg	ata	gca	2245																									
Leu	Met	Glu	Phe	Glu	Glu	Pro	His	Ala	Thr	Lys	Gln	Ser	Val	Ile	Ala																										
														430																											
ttg	ggc	tca	caa	gag	gga	gct	ctg	cat	caa	gct	ttg	gct	gga	gcc	att	2293																									
Leu	Gly	Ser	Gln	Glu	Gly	Ala	Leu	His	Gln	Ala	Leu	Ala	Gly	Ala	Ile																										
														450																											
cct	gtg	gaa	ttt	tca	agc	aac	act	gtc	aag	ttg	acg	tcg	ggt	cat	ttg	2341																									
Pro	Val	Glu	Phe	Ser	Ser	Asn	Thr	Val	Lys	Leu	Thr	Ser	Gly	His	Leu																										
														465																											
aag	tgt	aga	gtg	aag	atg	gaa	aaa	ttg	cag	ttg	aag	gga	aca	acc	tat	2389																									
Lys	Cys	Arg	Val	Lys	Met	Glu	Lys	Leu	Gln	Leu	Lys	Gly	Thr	Thr	Tyr																										
														480																											
ggc	gtc	tgt	tca	aag	gct	ttc	aag	ttt	ctt	ggg	act	ccc	gcg	gac	aca	2437																									
Gly	Val	Cys	Ser	Lys	Ala	Phe	Lys	Phe	Leu	Gly	Thr	Pro	Ala	Asp	Thr																										
														495																											
ggt	cac	ggc	act	gtg	gtg	ttg	gaa	ttg	cag	tac	act	ggc	acg	gat	gga	2485																									
Gly	His	Gly	Thr	Val	Val	Leu	Glu	Leu	Gln	Tyr	Thr	Gly	Thr	Asp	Gly																										
														510																											
cct	tgc	aaa	gtt	cct	atc	tcg	tca	gtg	gct	tca	ttg	aac	gac	cta	acg	2533																									
Pro	Cys	Lys	Val	Pro	Ile	Ser	Ser	Val	Ala	Ser	Leu	Asn	Asp	Leu	Thr																										
														530																											
cca	gtg	ggc	aga	ttg	gtc	act	gtc	aac	cct	ttt	gtt	tca	gtg	gcc	acg	2581																									

811252

Pro	Val	Gly	Arg	Leu	Val	Thr	Val	Asn	Pro	Phe	Val	Ser	Val	Ala	Thr		
			545					550					555				
gcc	aac	gct	aag	gtc	ctg	att	gaa	ttg	gaa	cca	ccc	ttt	gga	gac	tca	2629	
Ala	Asn	Ala	Lys	Val	Leu	Ile	Glu	Leu	Glu	Pro	Pro	Phe	Gly	Asp	Ser		
		560					565					570					
tac	ata	gtg	gtg	ggc	aga	gga	gaa	caa	cag	atc	aat	cac	cat	tgg	cac	2677	
Tyr	Ile	Val	Val	Gly	Arg	Gly	Glu	Gln	Gln	Ile	Asn	His	His	Trp	His		
	575					580					585						
aag	tct	gga	agc	agc	att	ggc	aaa	gcc	ttt	aca	acc	acc	ctc	aaa	gga	2725	
Lys	Ser	Gly	Ser	Ser	Ile	Gly	Lys	Ala	Phe	Thr	Thr	Thr	Leu	Lys	Gly		
590					595					600					605		
gcg	cag	aga	cta	gcc	gct	cta	gga	gac	aca	gct	tgg	gac	ttt	gga	tca	2773	
Ala	Gln	Arg	Leu	Ala	Ala	Leu	Gly	Asp	Thr	Ala	Trp	Asp	Phe	Gly	Ser		
				610					615					620			
gtt	gga	ggg	gtg	ttc	acc	tca	gtt	ggg	aag	gct	gtc	cat	caa	gtg	ttc	2821	
Val	Gly	Gly	Val	Phe	Thr	Ser	Val	Gly	Lys	Ala	Val	His	Gln	Val	Phe		
			625					630					635				
gga	gga	gca	ttc	cgc	tca	ctg	ttc	gga	ggc	atg	tcc	tgg	ata	acg	caa	2869	
Gly	Gly	Ala	Phe	Arg	Ser	Leu	Phe	Gly	Gly	Met	Ser	Trp	Ile	Thr	Gln		
		640					645					650					
gga	ttg	ctg	ggg	gct	ctc	ctg	ttg	tgg	atg	ggc	atc	aat	gct	cgt	gat	2917	
Gly	Leu	Leu	Gly	Ala	Leu	Leu	Leu	Trp	Met	Gly	Ile	Asn	Ala	Arg	Asp		
	655					660					665						
agg	tcc	ata	gct	ctc	acg	ttt	ctc	gca	gtt	gga	gga	gtt	ctg	ctc	ttc	2965	
Arg	Ser	Ile	Ala	Leu	Thr	Phe	Leu	Ala	Val	Gly	Gly	Val	Leu	Leu	Phe		
670					675					680					685		
ctc	tcc	gtg	aac	gtg	cac	gcc	tga	aggcggc	cgctcgagca	tgc	atctaga					3016	
Leu	Ser	Val	Asn	Val	His	Ala											
			690														
gggccctatt	ctatagtgtc	acctaaatgc	tagagctcgc	tgatcagcct	cgactgtgcc											3076	
ttctagtgtc	cagccatctg	ttgtttgccc	ctccccgtg	ccttccttga	ccctggaagg											3136	
tgccactccc	actgtccttt	cctaataaaa	tgaggaaatt	gcatcgcatt	gtctgagtag											3196	
gtgtcattct	attctggggg	gtgggggtggg	gcaggacagc	aagggggagg	attgggaaga											3256	
caatagcagg	catgctgggg	atgcggtggg	ctctatggct	tctgaggcgg	aaagaaccag											3316	
ctgcattaat	gaatcggcc	acgcgcgggg	agaggcgggt	tgcgtattgg	gcgctcttcc											3376	
gcttcctcgc	tactgactc	gctgcgctcg	gtcgttcggc	tgcggcgagc	ggatcagct											3436	
cactcaaagg	cggtaatacg	gttatccaca	gaatcagggg	ataacgcagg	aaagaacatg											3496	
tgagcaaaaag	gccagcaaaa	ggccaggaac	cgtaaaaagg	ccgcgttgct	ggcgtttttc											3556	
cataggctcc	gccccctga	cgagcatcac	aaaaatcgac	gctcaagtca	gaggtggcga											3616	
aaccgacag	gactataaag	ataccaggcg	tttccccctg	gaagctccct	cgtgcgctct											3676	
cctgttccga	ccctgccgct	taccggatac	ctgtccgcct	ttctcccttc	gggaagcgtg											3736	

811252

gcgctttctc atagctcacg ctgtaggtat ctcagttcgg ttaggtcgt tcgctccaag	3796
ctgggctgtg tgcacgaacc ccccgttcag cccgaccgct gcgccttata cggtaactat	3856
cgtcttgagt ccaacccggt aagacacgac ttatcgccac tggcagcagc cactggtaac	3916
aggattagca gagcgaggta ttaggcgggt gctacagagt tcttgaagtg gtggcctaac	3976
tacggctaca ctagaagaac agtatttggg atctgcgctc tgctgaagcc agttaccttc	4036
ggaaaaagag ttggtagctc ttgatccggc aaacaaacca ccgctggtag cgggtggtttt	4096
tttgtttgca agcagcagat tacgcgcaga aaaaaaggat ctcaagaaga tcctttgatc	4156
ttttctacgg ggtctgacgc tcagtggaac gaaaactcac gttaagggat tttggtcatg	4216
agattatcaa aaaggatctt cacctagatc cttttaaat aaaaatgaag ttttaaatca	4276
atctaaagta tatatgagta aacttgggtc gacagttacc aatgcttaat cagtgaggca	4336
cctatctcag cgatctgtct atttcgttca tccatagttg cctgactccc cgctcgttag	4396
ataactacga tacgggaggg cttaccatct ggccccagtg ctgcaatgat accgcgagac	4456
ccacgctcac cggctccaga tttatcagca ataaaccagc cagccggaag ggccgagcgc	4516
agaagtggtc ctgcaacttt atccgcctcc atccagtcta ttaattgttg ccgggaagct	4576
agagtaagta gttcgccagt taatagtttg cgcaacgttg ttgccattgc tacaggcatc	4636
gtggtgtcac gctcgtcgtt tggatgggt tcattcagct ccggttcca acgatcaagg	4696
cgagttacat gatcccccat gttgtgcaaa aaagcgggta gtccttcgg tcctccgatc	4756
gttgtcagaa gtaagttggc cgcagtgtta tcaactatgg ttatggcagc actgcataat	4816
tctcttactg tcatgccatc cgtaagatgc ttttctgtga ctggtgagta ctcaaccaag	4876
tcattctgag aatagtgtat gcggcgaccg agttgctctt gcccggcgtc aatacgggat	4936
aataccgctc cacatagcag aactttaaaa gtgctcatca ttggaaaacg ttcttcgggg	4996
cgaaaactct caaggatctt accgctgttg agatccagtt cgatgtaacc cactcgtgca	5056
cccaactgat cttcagcatc ttttactttc accagcgttt ctgggtgagc aaaaacagga	5116
aggcaaaatg ccgcaaaaaa gggaataagg gcgacacgga aatgttgaat actcatactc	5176
ttcctttttc aatattattg aagcatttat caggggttatt gtctcatgag cggatacata	5236
tttgaatgta tttagaaaaa taaacaaata ggggttccgc gcacatttcc ccgaaaagtg	5296
ccacctgacg tc	5308

<210> 16
 <211> 692
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic Construct

811252

<400> 16

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn Phe Gln Gly
20 25 30

Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp Val Ile Thr
35 40 45

Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg Ala Met Asp
50 55 60

Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys Pro Val Leu
65 70 75 80

Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Thr Lys Ser
85 90 95

Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg His Ser Arg
100 105 110

Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu Ser Thr Leu
115 120 125

Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala Thr Arg Tyr
130 135 140

Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly Tyr Ala Leu
145 150 155 160

Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr Met Gln Arg
165 170 175

Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe
180 185 190

Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser Gly
195 200 205

Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr Ile
210 215 220

Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met Glu
225 230 235 240

Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr Val
Page 19

245 811252 255
 Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala His
 260 265 270
 Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val Val
 275 280 285
 Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile
 290 295 300
 Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg Thr
 305 310 315 320
 Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly
 325 330 335
 Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly Ala
 340 345 350
 Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr Thr
 355 360 365
 Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro Arg
 370 375 380
 Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr Lys
 385 390 395 400
 Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro Trp
 405 410 415
 Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met Glu
 420 425 430
 Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala Leu Gly Ser
 435 440 445
 Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val Glu
 450 455 460
 Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg
 465 470 475 480
 Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val Cys
 485 490 495

Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His Gly
 500 505 510

Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys Lys
 515 520 525

Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val Gly
 530 535 540

Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn Ala
 545 550 555 560

Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val
 565 570 575

Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser Gly
 580 585 590

Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly Ala Gln Arg
 595 600 605

Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly
 610 615 620

Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly Ala
 625 630 635 640

Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu
 645 650 655

Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile
 660 665 670

Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser Val
 675 680 685

Asn Val His Ala
 690

<210> 17
 <211> 5334
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct

<220>
 <221> misc_feature

811252

<222> (1)..(5334)

<223> pCBE 1-14

<220>

<221> CDS

<222> (916)..(3006)

<400> 17

```

gacggatcgg gagatctccc gatccccctat ggtgcactct cagtacaatc tgctctgatg      60
ccgcatagtt aagccagtat ctgctccctg cttgtgtggt ggaggtcgct gagtagtgcg      120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180
ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240
gattattgac tagttattaa tagtaatcaa ttacgggggtc attagttcat agcccatata      300
tggagttccg cgttacataa cttacggtaa atggcccgcg tggctgaccg cccaacgacc      360
ccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420
attgacgtca atgggtggag tatttacggg aaactgcccc cttggcagta catcaagtgt      480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt      540
atgccagta catgacctta tgggactttc ctacttgga gtacatctac gtattagtca      600
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg      660
actcacgggg atttccaagt ctccaccca ttgacgtcaa tgggagtttg ttttggcacc      720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc ccattgacg caaatgggcg      780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaacca      840
ctgcttactg gcttatcgaa attaatacga ctactatag ggagaccaa gcttggtacc      900
tctagagccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa      951
          Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu
          1          5          10

ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg      999
Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
          15          20          25

gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc      1047
Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
          30          35          40

aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga      1095
Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly
          45          50          55          60

gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag      1143
Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu
          65          70          75

gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca      1191
Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro
          80          85          90

gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat      1239

```

																811252				
Glu	Asp	Val	Asp	Cys	Trp	Cys	Asp	Asn	Gln	Glu	Val	Tyr	Val	Gln	Tyr					
		95					100					105								
gga	cgg	tgc	acg	cgg	acc	agg	cat	tcc	aag	cga	agc	agg	aga	tcc	gtg	1287				
Gly	Arg	Cys	Thr	Arg	Thr	Arg	His	Ser	Lys	Arg	Ser	Arg	Arg	Ser	Val					
		110					115					120								
tcg	gtc	caa	aca	cat	ggg	gag	agt	tca	cta	gtg	aat	aaa	aaa	gag	gct	1335				
Ser	Val	Gln	Thr	His	Gly	Glu	Ser	Ser	Leu	Val	Asn	Lys	Lys	Glu	Ala					
		125			130					135					140					
tgg	ctg	gat	tca	acg	aaa	gcc	aca	cga	tat	ctc	atg	aaa	act	gag	aac	1383				
Trp	Leu	Asp	Ser	Thr	Lys	Ala	Thr	Arg	Tyr	Leu	Met	Lys	Thr	Glu	Asn					
			145							150					155					
tgg	atc	ata	agg	aat	cct	ggc	tat	gct	ttc	ctg	gcg	gcg	gta	ctt	ggc	1431				
Trp	Ile	Ile	Arg	Asn	Pro	Gly	Tyr	Ala	Phe	Leu	Ala	Ala	Val	Leu	Gly					
			160					165							170					
tgg	atg	ctt	ggc	agt	aac	aac	ggt	caa	cgc	gtg	gta	ttt	acc	atc	ctc	1479				
Trp	Met	Leu	Gly	Ser	Asn	Asn	Gly	Gln	Arg	Val	Val	Phe	Thr	Ile	Leu					
		175					180					185								
ctg	ctg	ttg	gtc	gct	ccg	gct	tac	agt	ttt	aat	tgt	ctg	gga	atg	ggc	1527				
Leu	Leu	Leu	Val	Ala	Pro	Ala	Tyr	Ser	Phe	Asn	Cys	Leu	Gly	Met	Gly					
		190					195					200								
aat	cgt	gac	ttc	ata	gaa	gga	gcc	agt	gga	gcc	act	tgg	gtg	gac	ttg	1575				
Asn	Arg	Asp	Phe	Ile	Glu	Gly	Ala	Ser	Gly	Ala	Thr	Trp	Val	Asp	Leu					
		205			210					215					220					
gtg	ctg	gaa	gga	gat	agc	tgc	ttg	aca	atc	atg	gca	aac	gac	aaa	cca	1623				
Val	Leu	Glu	Gly	Asp	Ser	Cys	Leu	Thr	Ile	Met	Ala	Asn	Asp	Lys	Pro					
			225							230					235					
aca	ttg	gac	gtc	cgc	atg	att	aac	atc	gaa	gct	agc	caa	ctt	gct	gag	1671				
Thr	Leu	Asp	Val	Arg	Met	Ile	Asn	Ile	Glu	Ala	Ser	Gln	Leu	Ala	Glu					
			240					245							250					
gtc	aga	agt	tac	tgc	tat	cat	gct	tca	gtc	act	gac	atc	tcg	acg	gtg	1719				
Val	Arg	Ser	Tyr	Cys	Tyr	His	Ala	Ser	Val	Thr	Asp	Ile	Ser	Thr	Val					
		255					260					265								
gct	cgg	tgc	ccc	acg	act	gga	gaa	gcc	cac	aac	gag	aag	cga	gct	gat	1767				
Ala	Arg	Cys	Pro	Thr	Thr	Gly	Glu	Ala	His	Asn	Glu	Lys	Arg	Ala	Asp					
		270					275					280								
agt	agc	tat	gtg	tgc	aaa	caa	ggc	ttc	act	gac	cgt	ggg	tgg	ggc	aac	1815				
Ser	Ser	Tyr	Val	Cys	Lys	Gln	Gly	Phe	Thr	Asp	Arg	Gly	Trp	Gly	Asn					
		285			290					295					300					
gga	tgt	gga	ctt	ttc	ggg	aag	gga	agc	att	gac	aca	tgt	gca	aaa	ttc	1863				
Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile	Asp	Thr	Cys	Ala	Lys	Phe					
			305							310					315					
tcc	tgc	acc	agt	aaa	gcg	att	ggg	aga	aca	atc	cag	cca	gaa	aac	atc	1911				
Ser	Cys	Thr	Ser	Lys	Ala	Ile	Gly	Arg	Thr	Ile	Gln	Pro	Glu	Asn	Ile					
			320					325					330							
aaa	tac	gaa	gtt	ggc	att	ttt	gtg	cat	gga	acc	acc	act	tcg	gaa	aac	1959				
Lys	Tyr	Glu	Val	Gly	Ile	Phe	Val	His	Gly	Thr	Thr	Thr	Ser	Glu	Asn					
		335					340					345								

															811252	
cat	ggg	aat	tat	tca	gcg	caa	ggt	ggg	gcg	tcc	cag	gcg	gca	aag	ttt	2007
His	Gly	Asn	Tyr	Ser	Ala	Gln	Val	Gly	Ala	Ser	Gln	Ala	Ala	Lys	Phe	
	350					355					360					
aca	gta	aca	ccc	aat	gct	cct	tcg	ata	acc	ctc	aaa	ctt	ggt	gac	tac	2055
Thr	Val	Thr	Pro	Asn	Ala	Pro	Ser	Ile	Thr	Leu	Lys	Leu	Gly	Asp	Tyr	
365					370					375					380	
gga	gaa	gtc	aca	ctg	gac	tgt	gag	cca	agg	agt	gga	ctg	aac	act	gaa	2103
Gly	Glu	Val	Thr	Leu	Asp	Cys	Glu	Pro	Arg	Ser	Gly	Leu	Asn	Thr	Glu	
				385					390					395		
gcg	ttt	tac	gtc	atg	acc	gtg	ggg	tca	aag	tca	ttt	ctg	gtc	cat	agg	2151
Ala	Phe	Tyr	Val	Met	Thr	Val	Gly	Ser	Lys	Ser	Phe	Leu	Val	His	Arg	
			400					405					410			
gag	tgg	ttt	cat	gac	ctc	gct	ctc	ccc	tgg	acg	tcc	cct	tcg	agc	aca	2199
Glu	Trp	Phe	His	Asp	Leu	Ala	Leu	Pro	Trp	Thr	Ser	Pro	Ser	Ser	Thr	
		415					420					425				
gcg	tgg	aga	aac	aga	gaa	ctc	ctc	atg	gaa	ttt	gaa	gag	gcg	cac	gcc	2247
Ala	Trp	Arg	Asn	Arg	Glu	Leu	Leu	Met	Glu	Phe	Glu	Glu	Ala	His	Ala	
	430					435					440					
aca	aaa	cag	tcc	gtt	gtt	gct	ctt	ggg	tca	cag	gaa	gga	ggc	ctc	cat	2295
Thr	Lys	Gln	Ser	Val	Val	Ala	Leu	Gly	Ser	Gln	Glu	Gly	Gly	Leu	His	
445					450					455					460	
cag	gcg	ttg	gca	gga	gcc	atc	gtg	gtg	gag	tac	tca	agc	tca	gtg	aag	2343
Gln	Ala	Leu	Ala	Gly	Ala	Ile	Val	Val	Glu	Tyr	Ser	Ser	Ser	Val	Lys	
				465					470					475		
tta	aca	tca	ggc	cac	ctg	aaa	tgt	agg	ctg	aaa	atg	gac	aaa	ctg	gct	2391
Leu	Thr	Ser	Gly	His	Leu	Lys	Cys	Arg	Leu	Lys	Met	Asp	Lys	Leu	Ala	
			480					485					490			
ctg	aaa	ggc	aca	acc	tat	ggc	atg	tgt	aca	gaa	aaa	ttc	tcg	ttc	gcg	2439
Leu	Lys	Gly	Thr	Thr	Tyr	Gly	Met	Cys	Thr	Glu	Lys	Phe	Ser	Phe	Ala	
		495					500					505				
aaa	aat	ccg	gcg	gac	act	ggt	cac	gga	aca	ggt	gtc	att	gaa	ctc	tcc	2487
Lys	Asn	Pro	Ala	Asp	Thr	Gly	His	Gly	Thr	Val	Val	Ile	Glu	Leu	Ser	
	510					515					520					
tac	tct	ggg	agt	gat	ggc	ccc	tgc	aaa	att	ccg	att	gct	tcc	gtt	gcg	2535
Tyr	Ser	Gly	Ser	Asp	Gly	Pro	Cys	Lys	Ile	Pro	Ile	Ala	Ser	Val	Ala	
525					530					535					540	
agc	ctc	aat	gac	atg	acc	ccc	gtt	ggg	cgg	ctg	gtg	aca	gtg	aac	ccc	2583
Ser	Leu	Asn	Asp	Met	Thr	Pro	Val	Gly	Arg	Leu	Val	Thr	Val	Asn	Pro	
				545					550					555		
ttc	gtc	gcg	act	tcc	agt	gcc	agc	tca	aag	gtg	ctg	gtc	gag	atg	gaa	2631
Phe	Val	Ala	Thr	Ser	Ser	Ala	Ser	Ser	Lys	Val	Leu	Val	Glu	Met	Glu	
			560					565					570			
ccc	ccc	ttc	gga	gac	tcc	tac	atc	gta	ggt	gga	agg	gga	gac	aag	cag	2679
Pro	Pro	Phe	Gly	Asp	Ser	Tyr	Ile	Val	Val	Gly	Arg	Gly	Asp	Lys	Gln	
		575					580					585				
atc	aac	cac	cat	tgg	cac	aaa	gct	gga	agc	acg	ctg	ggc	aag	gcc	ttt	2727
Ile	Asn	His	His	Trp	His	Lys	Ala	Gly	Ser	Thr	Leu	Gly	Lys	Ala	Phe	
	590					595					600					

811252

tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc gac aca Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr 605 610 615 620	2775
gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata gga aaa Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys 625 630 635	2823
gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt ggg gga Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly 640 645 650	2871
atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc tgg atg Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met 655 660 665	2919
ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta gcc aca Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr 670 675 680	2967
ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct taattagttt Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala 685 690 695	3016
gagcggccgc tcgagcatgc atctagaggg ccctattcta tagtgtcacc taaatgctag	3076
agctcgctga tcagcctcga ctgtgccttc tagttgccag ccatctgttg tttgcccctc	3136
ccccgtgcct tccttgaccc tggaagggtgc cactcccact gtcctttcct aataaaatga	3196
ggaaattgca tcgcattgtc tgagtaggtg tcattctatt ctgggggggtg ggggtggggca	3256
ggacagcaag ggggaggatt gggaagacaa tagcaggcat gctgggggatg cggtgggctc	3316
tatggcttct gaggcggaaa gaaccagctg cattaatgaa tcggccaacg cgcggggaga	3376
ggcggtttgc gtattgggcg ctcttcgct tcctcgctca ctgactcgct gcgctcggtc	3436
gttcggctgc ggcgagcggc atcagctcac tcaaaggcgg taatacgggt atccacagaa	3496
tcaggggata acgcaggaaa gaacatgtga gcaaaaggcc agcaaaaggc caggaaccgt	3556
aaaaaggccg cgttgctggc gtttttccat aggctccgcc cccctgacga gcatcacaaa	3616
aatcgacgct caagtcagag gtggcgaaac ccgacaggac tataaagata ccaggcgttt	3676
ccccctggaa gctccctcgt gcgctctcct gttccgacct tgccgcttac cggatacctg	3736
tccgcctttc tcccttcggg aagcgtggcg ctttctcata gctcacgctg taggtatctc	3796
agttcggtgt aggtcgttcg ctccaagctg ggctgtgtgc acgaaccccc cgttcagccc	3856
gaccgctgcg ccttatccgg taactatcgt cttgagtcca acccggttaag acacgactta	3916
tcgccactgg cagcagccac tggtaacagg attagcagag cgaggatatgt aggcggtgct	3976
acagagttct tgaagtgggt gcctaactac ggctacacta gaagaacagt atttggtatc	4036
tgcgctctgc tgaagccagt taccttcgga aaaagagttg gtagctcttg atccggcaaa	4096
caaaccaccg ctggtagcgg tggttttttt gtttgcaagc agcagattac gcgcagaaaa	4156

811252

```

aaaggatctc aagaagatcc tttgatcttt tctacggggt ctgacgctca gtggaacgaa 4216
aactcacgtt aagggtatctt ggtcatgaga ttatcaaaaa ggatcttcac ctagatcctt 4276
ttaaattaaa aatgaagttt taaatcaatc taaagtatat atgagtaaag ttggtctgac 4336
agttaccaat gcttaatcag tgaggcacct atctcagcga tctgtctatt tcgttcatcc 4396
atagttgcct gactccccgt cgtgtagata actacgatac gggagggcctt accatctggc 4456
cccagtgctg caatgatacc gcgagacca cgcacacggg ctccagattt atcagcaata 4516
aaccagccag ccggaagggc cgagcgcaga agtggtcctg caactttatc cgcctccatc 4576
cagtctatta attgttgccg ggaagctaga gtaagtagtt cgccagttaa tagtttgccg 4636
aacgttggtg ccattgctac aggcacgtg gtgtcacgct cgtcgtttgg tatggcttca 4696
ttcagctccg gttcccaacg atcaaggcga gttacatgat ccccatgtt gtgcaaaaaa 4756
gcggttagct ccttcgggtc tccgatcgtt gtcagaagta agttggccgc agtggttatca 4816
ctcatgggta tggcagcact gcataattct cttactgtca tgccatccgt aagatgcttt 4876
tctgtgactg gtgagtactc aaccaagtca ttctgagaat agtgtatgcg gcgaccgagt 4936
tgctcttgcc cggcgtcaat acgggataat accgcgccac atagcagaac tttaaaagtg 4996
ctcatcattg gaaaacgttc ttcggggcga aaactctcaa ggatcttacc gctgttgaga 5056
tccagttcga tgtaaccac tcgtgcacc aactgatctt cagcatcttt tactttcacc 5116
agcgtttctg ggtgagcaaa aacaggaagg caaatgccg caaaaaagg aataagggcg 5176
acacggaaat gttgaatact catactcttc ctttttcaat attattgaag catttatcag 5236
ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa acaaataagg 5296
gttccgcgca ctttccccg aaaagtgcc cctgacgt 5334

```

<210> 18
 <211> 697
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 18

Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met
 1 5 10 15

Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys
 20 25 30

Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp
 35 40 45

Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys
 50 55 60

Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr
 65 70 75 80

Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp
 85 90 95

Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr
 100 105 110

Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr
 115 120 125

His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser
 130 135 140

Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg
 145 150 155 160

Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly
 165 170 175

Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Leu Val
 180 185 190

Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe
 195 200 205

Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly
 210 215 220

Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val
 225 230 235 240

Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr
 245 250 255

Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro
 260 265 270

Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val
 275 280 285

Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
 290 295 300

811252

Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser
305 310 315 320

Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val
325 330 335

Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr
340 345 350

Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro
355 360 365

Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr
370 375 380

Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val
385 390 395 400

Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His
405 410 415

Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn
420 425 430

Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser
435 440 445

Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala
450 455 460

Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly
465 470 475 480

His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr
485 490 495

Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala
500 505 510

Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser
515 520 525

Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp
530 535 540

Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr
545 550 555 560

811252

Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly
565 570 575

Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His
580 585 590

Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu
595 600 605

Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe
610 615 620

Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln
625 630 635 640

Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile
645 650 655

Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala
660 665 670

Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu
675 680 685

Val Phe Leu Ala Thr Asn Val His Ala
690 695

<210> 19
<211> 5283
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> CDS
<222> (910)..(2964)

<400> 19
gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg 60
ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
ttagggtttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240
gattattgac tagttattaa tagtaatcaa ttacgggggtc attagttcat agcccatata 300
tggagttccg cgttacataa cttacggtaa atggcccggc tggctgaccg cccaacgacc 360

811252

cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc	420
attgacgtca atgggtggac tatttacggt aaactgcca cttggcagta catcaagtgt	480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt	540
atgcccagta catgacctta tgggactttc ctacttgga gtacatctac gtattagtca	600
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg	660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc	720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg	780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaacca	840
ctgcttactg gcttatcgaa attaatacga ctactatag ggagaccaa gcttggtacc	900
gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc	951
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser	
1 5 10	
ttg gca gtt gtc ata gct ggt aca agc gct acc acc atc cac cgg gac	999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Thr Thr Ile His Arg Asp	
15 20 25 30	
agg gaa gga tac atg gtt atg cgg gcc agt gga agg gac gct gca agc	1047
Arg Glu Gly Tyr Met Val Met Arg Ala Ser Gly Arg Asp Ala Ala Ser	
35 40 45	
cag gtc agg gta caa aac gga acg tgc gtc atc ctg gca aca gac atg	1095
Gln Val Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met	
50 55 60	
gga gag tgg tgt gaa gat tca atc acc tac tct tgc gtc acg att gac	1143
Gly Glu Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp	
65 70 75	
cag gag gaa gaa ccc gtt gac gtg gac tgc ttc tgc cga ggt gtt gat	1191
Gln Glu Glu Glu Pro Val Asp Val Asp Cys Phe Cys Arg Gly Val Asp	
80 85 90	
agg gtt aag tta gag tat gga cgc tgt gga agg caa gct gga tct agg	1239
Arg Val Lys Leu Glu Tyr Gly Arg Cys Gly Arg Gln Ala Gly Ser Arg	
95 100 105 110	
ggg aaa agg tct gtg gtc att cca aca cat gca caa aaa gac atg gtc	1287
Gly Lys Arg Ser Val Val Ile Pro Thr His Ala Gln Lys Asp Met Val	
115 120 125	
ggg cga ggt cat gca tgg ctt aaa ggt gac aat att cga gat cat gtc	1335
Gly Arg Gly His Ala Trp Leu Lys Gly Asp Asn Ile Arg Asp His Val	
130 135 140	
acc cga gtc gag ggc tgg atg tgg aag aac aag ctt cta act gcc gcc	1383
Thr Arg Val Glu Gly Trp Met Trp Lys Asn Lys Leu Leu Thr Ala Ala	
145 150 155	
att gtg gcc ttg gct tgg ctc atg gtt gat agt tgg atg gcc aga gtg	1431
Ile Val Ala Leu Ala Trp Leu Met Val Asp Ser Trp Met Ala Arg Val	
160 165 170	

															811252	
act	gtc	atc	ctc	ttg	gcg	ttg	agt	cta	ggg	cca	gtg	tac	gcc	acg	agg	1479
Thr	Val	Ile	Leu	Leu	Ala	Leu	Ser	Leu	Gly	Pro	Val	Tyr	Ala	Thr	Arg	190
175					180					185						
tgc	acg	cat	ctt	gag	aac	aga	gat	ttt	gtg	aca	gga	act	caa	ggg	acc	1527
Cys	Thr	His	Leu	Glu	Asn	Arg	Asp	Phe	Val	Thr	Gly	Thr	Gln	Gly	Thr	205
				195					200					205		
acc	aga	gtg	tcc	cta	gtt	ttg	gaa	ctt	gga	ggc	tgc	gtg	acc	atc	aca	1575
Thr	Arg	Val	Ser	Leu	Val	Leu	Glu	Leu	Gly	Gly	Cys	Val	Thr	Ile	Thr	220
			210					215								
gct	gag	ggc	aag	cca	tcc	att	gat	gta	tgg	ctc	gaa	gac	att	ttt	cag	1623
Ala	Glu	Gly	Lys	Pro	Ser	Ile	Asp	Val	Trp	Leu	Glu	Asp	Ile	Phe	Gln	235
		225					230									
gaa	agc	ccg	gct	gaa	acc	aga	gaa	tac	tgc	ctg	cac	gcc	aaa	ttg	acc	1671
Glu	Ser	Pro	Ala	Glu	Thr	Arg	Glu	Tyr	Cys	Leu	His	Ala	Lys	Leu	Thr	250
	240					245										
aac	aca	aaa	gtg	gag	gct	cgc	tgt	cca	acc	act	gga	ccg	gcg	aca	ctt	1719
Asn	Thr	Lys	Val	Glu	Ala	Arg	Cys	Pro	Thr	Thr	Gly	Pro	Ala	Thr	Leu	270
255					260					265						
ccg	gag	gag	cat	cag	gct	aat	atg	gtg	tgc	aag	aga	gac	caa	agc	gac	1767
Pro	Glu	Glu	His	Gln	Ala	Asn	Met	Val	Cys	Lys	Arg	Asp	Gln	Ser	Asp	285
				275					280					285		
cgt	gga	tgg	gga	aac	cac	tgc	ggg	ttt	ttt	ggg	aag	ggc	agt	ata	gtg	1815
Arg	Gly	Trp	Gly	Asn	His	Cys	Gly	Phe	Phe	Gly	Lys	Gly	Ser	Ile	Val	300
			290					295								
gct	tgt	gca	aag	ttt	gaa	tgc	gag	gaa	gca	aaa	aaa	gct	gtg	ggc	cac	1863
Ala	Cys	Ala	Lys	Phe	Glu	Cys	Glu	Glu	Ala	Lys	Lys	Ala	Val	Gly	His	315
		305					310									
gtc	tat	gac	tcc	aca	aag	atc	acg	tat	gtt	gtc	aag	gtt	gag	ccc	cac	1911
Val	Tyr	Asp	Ser	Thr	Lys	Ile	Thr	Tyr	Val	Val	Lys	Val	Glu	Pro	His	330
	320					325										
aca	ggg	gat	tac	ttg	gct	gca	aat	gag	acc	aat	tca	aac	agg	aaa	tca	1959
Thr	Gly	Asp	Tyr	Leu	Ala	Ala	Asn	Glu	Thr	Asn	Ser	Asn	Arg	Lys	Ser	350
335					340					345						
gca	cag	ttt	acg	gtg	gca	tcc	gag	aaa	gtg	atc	ctg	cgg	ctc	ggc	gac	2007
Ala	Gln	Phe	Thr	Val	Ala	Ser	Glu	Lys	Val	Ile	Leu	Arg	Leu	Gly	Asp	365
				355					360					365		
tat	gga	gat	gtg	tcg	ctg	acg	tgt	aaa	gtg	gca	agt	ggg	att	gat	gtc	2055
Tyr	Gly	Asp	Val	Ser	Leu	Thr	Cys	Lys	Val	Ala	Ser	Gly	Ile	Asp	Val	380
			370					375								
gcc	caa	act	gtg	gtg	atg	tca	ctc	gac	agc	agc	aag	gac	cac	ctg	cct	2103
Ala	Gln	Thr	Val	Val	Met	Ser	Leu	Asp	Ser	Ser	Lys	Asp	His	Leu	Pro	395
		385					390									
tct	gca	tgg	caa	gtg	cac	cgt	gac	tgg	ttt	gag	gac	ttg	gcg	ctg	ccc	2151
Ser	Ala	Trp	Gln	Val	His	Arg	Asp	Trp	Phe	Glu	Asp	Leu	Ala	Leu	Pro	410
	400					405										
tgg	aaa	cac	aag	gac	aac	caa	gat	tgg	aac	agt	gtg	gag	aaa	ctt	gtg	2199
Trp	Lys	His	Lys	Asp	Asn	Gln	Asp	Trp	Asn	Ser	Val	Glu	Lys	Leu	Val	430
415					420					425					430	

811252

gaa ttt gga cca cca cat gct gtg aaa atg gat gtt ttc aat ctg ggg Glu Phe Gly Pro Pro His Ala Val Lys Met Asp Val Phe Asn Leu Gly 435 440 445	2247
gac cag acg gct gtg ctg ctc aaa tca ctg gca gga gtt ccg ctg gcc Asp Gln Thr Ala Val Leu Leu Lys Ser Leu Ala Gly Val Pro Leu Ala 450 455 460	2295
agt gtg gag ggc cag aaa tac cac ctg aaa agc ggc cat gtt act tgt Ser Val Glu Gly Gln Lys Tyr His Leu Lys Ser Gly His Val Thr Cys 465 470 475	2343
gat gtg gga ctg gaa aag ctg aaa ctg aaa ggc aca acc tac tcc atg Asp Val Gly Leu Glu Lys Leu Lys Leu Lys Gly Thr Thr Tyr Ser Met 480 485 490	2391
tgt gac aaa gca aag ttc aaa tgg aag aga gtt cct gtg gac agc ggc Cys Asp Lys Ala Lys Phe Lys Trp Lys Arg Val Pro Val Asp Ser Gly 495 500 505 510	2439
cat gac aca gta gtc atg gag gta tca tac aca gga agc gac aag cca His Asp Thr Val Val Met Glu Val Ser Tyr Thr Gly Ser Asp Lys Pro 515 520 525	2487
tgt cgg atc ccg gtg cgg gct gtg gca cat ggt gtc cca gcg gtt aat Cys Arg Ile Pro Val Arg Ala Val Ala His Gly Val Pro Ala Val Asn 530 535 540	2535
gta gcc atg ctc ata acc ccc aat cca acc att gaa aca aat ggt ggc Val Ala Met Leu Ile Thr Pro Asn Pro Thr Ile Glu Thr Asn Gly Gly 545 550 555	2583
gga ttc ata gaa atg cag ctg cca cca ggg gat aac atc atc tat gtg Gly Phe Ile Glu Met Gln Leu Pro Pro Gly Asp Asn Ile Ile Tyr Val 560 565 570	2631
gga gac ctt agc cag cag tgg ttt cag aaa ggc agt acc att ggt aga Gly Asp Leu Ser Gln Gln Trp Phe Gln Lys Gly Ser Thr Ile Gly Arg 575 580 585 590	2679
atg ttt gaa aaa acc cgc agg gga ttg gaa agg ctc tct gtg gtt gga Met Phe Glu Lys Thr Arg Arg Gly Leu Glu Arg Leu Ser Val Val Gly 595 600 605	2727
gaa cat gca tgg gac ttt ggc tca gta ggc ggg gta ctg tct tct gtg Glu His Ala Trp Asp Phe Gly Ser Val Gly Gly Val Leu Ser Ser Val 610 615 620	2775
ggg aag gca atc cac acg gtg ctg ggg gga gct ttc aac acc ctt ttt Gly Lys Ala Ile His Thr Val Leu Gly Gly Ala Phe Asn Thr Leu Phe 625 630 635	2823
ggg ggg gtt gga ttc atc cct aag atg ctg ctg ggg gtt gct ctg gtc Gly Gly Val Gly Phe Ile Pro Lys Met Leu Leu Gly Val Ala Leu Val 640 645 650	2871
tgg ttg gga cta aat gcc agg aat cca acg atg tcc atg acg ttt ctt Trp Leu Gly Leu Asn Ala Arg Asn Pro Thr Met Ser Met Thr Phe Leu 655 660 665 670	2919
gct gtg ggg gct ttg aca ctg atg atg aca atg gga gtt ggg gca Ala Val Gly Ala Leu Thr Leu Met Met Thr Met Gly Val Gly Ala 675 680 685 690	2964

			811252			
675		680		685		
tgagcgccg	ctcgagcatg	catctagagg	gccctattct	atagtgtcac	ctaaatgcta	3024
gagctcgctg	atcagcctcg	actgtgcctt	ctagttgcc	gccatctgtt	gtttgccct	3084
ccccgtgcc	ttccttgacc	ctggaagggtg	ccactccac	tgtcctttcc	taataaaatg	3144
aggaaattgc	atcgcatgtg	ctgagtaggt	gtcattctat	tctggggggt	ggggtggggc	3204
aggacagcaa	gggggaggat	tgggaagaca	atagcaggca	tgctggggat	gcggtgggct	3264
ctatggcttc	tgaggcggaa	agaacagctg	cattaatgaa	tcggccaacg	cgcggggaga	3324
ggcggtttgc	gtattgggcg	ctcttccgct	tctcgtca	ctgactcgt	gcgctcggtc	3384
gttcggctgc	ggcgagcggg	atcagctcac	tcaaaggcgg	taatacgggt	atccacagaa	3444
tcaggggata	acgcaggaaa	gaacatgtga	gcaaaaggcc	agcaaaaggc	caggaaccgt	3504
aaaaaggccg	cgttgctggc	gtttttccat	aggctccgcc	cccctgacga	gcatcacaaa	3564
aatcgacgct	caagtcagag	gtggcgaaac	ccgacaggac	tataaagata	ccaggcgttt	3624
cccctggaa	gctccctcgt	gcgctctcct	gttccgacct	tgccgcttac	cggataacctg	3684
tccgcctttc	tcccttcggg	aagcgtggcg	ctttctcaat	gctcacgctg	taggtatctc	3744
agttcggtgt	aggctggtcg	ctccaagctg	ggctgtgtgc	acgaaccccc	cgttcagccc	3804
gaccgctgcg	ccttatccgg	taactatcgt	cttgagtcca	acccggtaa	acacgactta	3864
tcgccactgg	cagcagccac	tggtaacagg	attagcagag	cgaggatatgt	aggcggtgct	3924
acagagttct	tgaagtgggtg	gcctaactac	ggctacacta	gaaggacagt	atttggtatc	3984
tgcgctctgc	tgaagccagt	taccttcgga	aaaagagttg	gtagctcttg	atccggcaaa	4044
caaaccaccg	ctggtagcgg	tggttttttt	gtttgcaagc	agcagattac	gcgcagaaaa	4104
aaaggatctc	aagaagatcc	tttgatcttt	tctacggggt	ctgacgctca	gtggaacgaa	4164
aactcacgtt	aagggtatctt	ggcatgaga	ttatcaaaaa	ggatcttcac	ctagatcctt	4224
ttaaattaaa	aatgaagttt	taaatcaatc	taaagtatat	atgagtaaac	ttggtctgac	4284
agttaccaat	gcttaatcag	tgaggcacct	atctcagcga	tctgtctatt	tcgttcatcc	4344
atagttgcct	gactccccgt	cgtgtagata	actacgatac	gggagggctt	accatctggc	4404
cccagtgtg	caatgatacc	gcgagacca	cgctcaccgg	ctccagatctt	atcagcaata	4464
aaccagccag	ccggaagggc	cgagcgcaga	agtggtcctg	caactttatc	cgctccatc	4524
cagtctatta	attggtgccg	ggaagctaga	gtaagtagtt	cgccagttaa	tagtttgccg	4584
aacgttggtg	ccattgctac	aggcatcgtg	gtgtcacgct	cgctggttg	tatggcttca	4644
ttcagctccg	gttcccaacg	atcaaggcga	gttacatgat	ccccatggt	gtgcaaaaaa	4704
gcggttagct	ccttcgggtc	tccgatcgtt	gtcagaagta	agttggccgc	agtgttatca	4764
ctcatgggta	tggcagcact	gcataattct	cttactgtca	tgccatccgt	aagatgcttt	4824

811252

tctgtgactg gtgagtactc aaccaagtca ttctgagaat agtgtatgcg gcgaccgagt	4884
tgctcttgcc cggcgtcaat acgggataat accgcgccac atagcagaac tttaaaagtg	4944
ctcatcattg gaaaacgttc ttcggggcga aaactctcaa ggatcttacc gctgttgaga	5004
tccagttcga tgtaaccac tcgtgcaccc aactgatctt cagcatcttt tactttcacc	5064
agcgtttctg ggtgagcaaa aacaggaagg caaaatgccg caaaaaaggg aataagggcg	5124
acacggaaat gttgaatact catactcttc ctttttcaat attattgaag catttatcag	5184
ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa acaaataggg	5244
gttccgcgca catttccccg aaaagtgcc cctgacgtc	5283

<210> 20
 <211> 685
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 20

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala	
1 5 10 15	

Val Val Ile Ala Gly Thr Ser Ala Thr Thr Ile His Arg Asp Arg Glu	
20 25 30	

Gly Tyr Met Val Met Arg Ala Ser Gly Arg Asp Ala Ala Ser Gln Val	
35 40 45	

Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met Gly Glu	
50 55 60	

Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp Gln Glu	
65 70 75 80	

Glu Glu Pro Val Asp Val Asp Cys Phe Cys Arg Gly Val Asp Arg Val	
85 90 95	

Lys Leu Glu Tyr Gly Arg Cys Gly Arg Gln Ala Gly Ser Arg Gly Lys	
100 105 110	

Arg Ser Val Val Ile Pro Thr His Ala Gln Lys Asp Met Val Gly Arg	
115 120 125	

Gly His Ala Trp Leu Lys Gly Asp Asn Ile Arg Asp His Val Thr Arg	
130 135 140	

811252

Val Glu Gly Trp Met Trp Lys Asn Lys Leu Leu Thr Ala Ala Ile Val
145 150 155 160

Ala Leu Ala Trp Leu Met Val Asp Ser Trp Met Ala Arg Val Thr Val
165 170 175

Ile Leu Leu Ala Leu Ser Leu Gly Pro Val Tyr Ala Thr Arg Cys Thr
180 185 190

His Leu Glu Asn Arg Asp Phe Val Thr Gly Thr Gln Gly Thr Thr Arg
195 200 205

Val Ser Leu Val Leu Glu Leu Gly Gly Cys Val Thr Ile Thr Ala Glu
210 215 220

Gly Lys Pro Ser Ile Asp Val Trp Leu Glu Asp Ile Phe Gln Glu Ser
225 230 235 240

Pro Ala Glu Thr Arg Glu Tyr Cys Leu His Ala Lys Leu Thr Asn Thr
245 250 255

Lys Val Glu Ala Arg Cys Pro Thr Thr Gly Pro Ala Thr Leu Pro Glu
260 265 270

Glu His Gln Ala Asn Met Val Cys Lys Arg Asp Gln Ser Asp Arg Gly
275 280 285

Trp Gly Asn His Cys Gly Phe Phe Gly Lys Gly Ser Ile Val Ala Cys
290 295 300

Ala Lys Phe Glu Cys Glu Glu Ala Lys Lys Ala Val Gly His Val Tyr
305 310 315 320

Asp Ser Thr Lys Ile Thr Tyr Val Val Lys Val Glu Pro His Thr Gly
325 330 335

Asp Tyr Leu Ala Ala Asn Glu Thr Asn Ser Asn Arg Lys Ser Ala Gln
340 345 350

Phe Thr Val Ala Ser Glu Lys Val Ile Leu Arg Leu Gly Asp Tyr Gly
355 360 365

Asp Val Ser Leu Thr Cys Lys Val Ala Ser Gly Ile Asp Val Ala Gln
370 375 380

Thr Val Val Met Ser Leu Asp Ser Ser Lys Asp His Leu Pro Ser Ala
385 390 395 400

811252

Trp Gln Val His Arg Asp Trp Phe Glu Asp Leu Ala Leu Pro Trp Lys
405 410 415

His Lys Asp Asn Gln Asp Trp Asn Ser Val Glu Lys Leu Val Glu Phe
420 425 430

Gly Pro Pro His Ala Val Lys Met Asp Val Phe Asn Leu Gly Asp Gln
435 440 445

Thr Ala Val Leu Leu Lys Ser Leu Ala Gly Val Pro Leu Ala Ser Val
450 455 460

Glu Gly Gln Lys Tyr His Leu Lys Ser Gly His Val Thr Cys Asp Val
465 470 475 480

Gly Leu Glu Lys Leu Lys Leu Lys Gly Thr Thr Tyr Ser Met Cys Asp
485 490 495

Lys Ala Lys Phe Lys Trp Lys Arg Val Pro Val Asp Ser Gly His Asp
500 505 510

Thr Val Val Met Glu Val Ser Tyr Thr Gly Ser Asp Lys Pro Cys Arg
515 520 525

Ile Pro Val Arg Ala Val Ala His Gly Val Pro Ala Val Asn Val Ala
530 535 540

Met Leu Ile Thr Pro Asn Pro Thr Ile Glu Thr Asn Gly Gly Gly Phe
545 550 555 560

Ile Glu Met Gln Leu Pro Pro Gly Asp Asn Ile Ile Tyr Val Gly Asp
565 570 575

Leu Ser Gln Gln Trp Phe Gln Lys Gly Ser Thr Ile Gly Arg Met Phe
580 585 590

Glu Lys Thr Arg Arg Gly Leu Glu Arg Leu Ser Val Val Gly Glu His
595 600 605

Ala Trp Asp Phe Gly Ser Val Gly Gly Val Leu Ser Ser Val Gly Lys
610 615 620

Ala Ile His Thr Val Leu Gly Gly Ala Phe Asn Thr Leu Phe Gly Gly
625 630 635 640

Val Gly Phe Ile Pro Lys Met Leu Leu Gly Val Ala Leu Val Trp Leu
Page 36

645 811252 655

Gly Leu Asn Ala Arg Asn Pro Thr Met Ser Met Thr Phe Leu Ala Val
660 665 670

Gly Ala Leu Thr Leu Met Met Thr Met Gly Val Gly Ala
675 680 685

<210> 21
<211> 5304
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> CDS
<222> (910)..(2985)

<400> 21
gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg 60
ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
ttagggttag gcgttttgcg ctgcttcgcy atgtacgggc cagatatacg cgttgacatt 240
gattattgac tagttattaa tagtaatcaa ttacgggggtc attagttcat agcccatata 300
tggagttccg cgttacataa cttacggtaa atggcccggc tggctgaccg cccaacgacc 360
cccggccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
attgacgtca atgggtggac tatttacggt aaactgcccc cttggcagta catcaagtgt 480
atcatatgcc aagtagcccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540
atgccagta catgacctta tgggactttc ctacttgga gtacatctac gtattagtca 600
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcy 780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaacca 840
ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttggtacc 900
gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
1 5 10
ttg gca gtt gtc ata gct ggt aca agc gct ttg cag tta tca acc tat 999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr
15 20 25 30

															811252	
cag	ggg	aaa	gtg	tta	atg	tca	atc	aac	aag	act	gac	gct	caa	agc	gcc	1047
Gln	Gly	Lys	Val	Leu	Met	Ser	Ile	Asn	Lys	Thr	Asp	Ala	Gln	Ser	Ala	
				35					40					45		
ata	aac	att	cct	agt	gcc	aac	gga	gca	aac	act	tgc	att	gtg	agg	gct	1095
Ile	Asn	Ile	Pro	Ser	Ala	Asn	Gly	Ala	Asn	Thr	Cys	Ile	Val	Arg	Ala	
			50					55					60			
cta	gat	gtg	ggg	gtc	atg	tgc	aaa	gat	gac	atc	aca	tac	ctg	tgc	cca	1143
Leu	Asp	Val	Gly	Val	Met	Cys	Lys	Asp	Asp	Ile	Thr	Tyr	Leu	Cys	Pro	
		65					70					75				
gtg	ctt	tca	gcg	gga	aat	gat	ccc	gag	gac	att	gac	tgt	tgg	tgt	gac	1191
Val	Leu	Ser	Ala	Gly	Asn	Asp	Pro	Glu	Asp	Ile	Asp	Cys	Trp	Cys	Asp	
	80					85					90					
gtc	gaa	gag	gtg	tgg	gtg	cac	tac	ggc	aga	tgc	acg	cgc	atg	gga	cat	1239
Val	Glu	Glu	Val	Trp	Val	His	Tyr	Gly	Arg	Cys	Thr	Arg	Met	Gly	His	
	95				100					105				110		
tcg	agg	cgt	agc	cga	cgg	tca	atc	tct	gtg	cag	cat	cat	gga	gat	tcc	1287
Ser	Arg	Arg	Ser	Arg	Arg	Ser	Ile	Ser	Val	Gln	His	His	Gly	Asp	Ser	
				115					120					125		
aca	ctg	gca	aca	aag	aac	acg	cca	tgg	ttg	gac	acc	gtg	aaa	acc	acc	1335
Thr	Leu	Ala	Thr	Lys	Asn	Thr	Pro	Trp	Leu	Asp	Thr	Val	Lys	Thr	Thr	
			130					135					140			
aaa	tac	ttg	aca	aaa	gta	gaa	aac	tgg	gtt	ttg	cgc	aat	cct	gga	tat	1383
Lys	Tyr	Leu	Thr	Lys	Val	Glu	Asn	Trp	Val	Leu	Arg	Asn	Pro	Gly	Tyr	
		145					150					155				
gcc	cta	gtt	gcg	ctg	gcg	att	gga	tgg	atg	ctc	ggt	agc	aac	aac	aca	1431
Ala	Leu	Val	Ala	Leu	Ala	Ile	Gly	Trp	Met	Leu	Gly	Ser	Asn	Asn	Thr	
	160					165					170					
cag	aga	gtg	gtt	ttt	gtg	atc	atg	ctg	atg	ctg	att	gct	ccg	gca	tac	1479
Gln	Arg	Val	Val	Phe	Val	Ile	Met	Leu	Met	Leu	Ile	Ala	Pro	Ala	Tyr	
					180					185					190	
agc	ttc	aac	tgt	ctg	gga	aca	tca	aac	agg	gac	ttt	gtc	gag	gga	gcc	1527
Ser	Phe	Asn	Cys	Leu	Gly	Thr	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Ala	
				195					200					205		
agt	ggg	gca	aca	tgg	att	gac	ttg	gta	ctt	gaa	ggg	gga	agc	tgt	gtc	1575
Ser	Gly	Ala	Thr	Trp	Ile	Asp	Leu	Val	Leu	Glu	Gly	Gly	Ser	Cys	Val	
			210					215					220			
aca	gtg	atg	gca	cca	gag	aaa	cca	aca	ctg	gac	ttc	aaa	gtg	atg	aag	1623
Thr	Val	Met	Ala	Pro	Glu	Lys	Pro	Thr	Leu	Asp	Phe	Lys	Val	Met	Lys	
			225				230					235				
atg	gag	gct	acc	gag	tta	gcc	act	gtg	cgt	gag	tat	tgt	tac	gaa	gca	1671
Met	Glu	Ala	Thr	Glu	Leu	Ala	Thr	Val	Arg	Glu	Tyr	Cys	Tyr	Glu	Ala	
			240			245					250					
acc	ttg	gac	acg	ctg	tca	aca	gtg	gca	agg	tgc	ccc	aca	aca	gga	gaa	1719
Thr	Leu	Asp	Thr	Leu	Ser	Thr	Val	Ala	Arg	Cys	Pro	Thr	Thr	Gly	Glu	
					260					265					270	
gct	cac	aac	acc	aaa	agg	agt	gac	cca	aca	ttt	gtc	tgc	aaa	aga	gat	1767
Ala	His	Asn	Thr	Lys	Arg	Ser	Asp	Pro	Thr	Phe	Val	Cys	Lys	Arg	Asp	
				275						280				285		

811252

gtt Val	gtg Val	gac Asp	cgc Arg 290	gga Gly	tgg Trp	ggt Gly	aac Asn	gga Gly 295	tgt Cys	ggt Gly	ctg Leu	ttt Phe	gga Gly 300	aaa Lys	ggg Gly	1815
agc Ser	att Ile	gac Asp 305	aca Thr	tgc Cys	gct Ala	aag Lys	ttc Phe 310	aca Thr	tgc Cys	aaa Lys	aac Asn	aag Lys 315	gca Ala	aca Thr	ggg Gly	1863
aag Lys	acg Thr 320	atc Ile	ttg Leu	aga Arg	gaa Glu	aac Asn 325	atc Ile	aag Lys	tat Tyr	gag Glu	gtt Val 330	gca Ala	atc Ile	ttt Phe	gtg Val	1911
cat His 335	ggt Gly	tca Ser	acg Thr	gac Asp	tct Ser 340	acg Thr	tca Ser	cat His	ggc Gly 345	aat Asn	tac Tyr	tct Ser	gag Glu	cag Gln	att Ile 350	1959
gga Gly	aaa Lys	aac Asn	caa Gln 355	gcg Ala	gct Ala	aga Arg	ttc Phe	acc Thr	ata Ile 360	agc Ser	ccg Pro	caa Gln	gca Ala	ccg Pro 365	tcc Ser	2007
ttt Phe	acg Thr	gcc Ala 370	aac Asn	atg Met	ggc Gly	gag Glu	tat Tyr	gga Gly 375	aca Thr	gtt Val	acc Thr	att Ile 380	gat Asp	tgt Cys	gaa Glu	2055
gca Ala	aga Arg 385	tca Ser	gga Gly	atc Ile	aac Asn	acg Thr	gag Glu 390	gat Asp	tat Tyr	tat Tyr	gtt Val	ttc Phe 395	act Thr	gtc Val	aag Lys	2103
gag Glu 400	aag Lys	tca Ser	tgg Trp	cta Leu	gtg Val	aac Asn 405	agg Arg	gac Asp	tgg Trp	ttt Phe	cac His 410	gac Asp	ttg Leu	aac Asn	ctt Leu	2151
cca Pro 415	tgg Trp	acg Thr	agc Ser	cct Pro	gcc Ala 420	aca Thr	act Thr	gat Asp	tgg Trp	cgc Arg 425	aac Asn	aga Arg	gaa Glu	aca Thr	ctg Leu 430	2199
gtg Val	gaa Glu	ttt Phe	gag Glu 435	gaa Glu	ccg Pro	cat His	gcc Ala	acc Thr	aag Lys 440	caa Gln	act Thr	gta Val	gta Val	gcc Ala 445	cta Leu	2247
gga Gly	tcg Ser	caa Gln 450	gaa Glu	ggt Gly	gcc Ala	ctg Leu	cac His 455	aca Thr 455	gca Ala	ttg Leu	gct Ala	gga Gly 460	gcc Ala 460	att Ile	cca Pro	2295
gcc Ala	act Thr 465	gtt Val	agc Ser	agc Ser	tca Ser	acc Thr	cta Leu 470	acc Thr	ttg Leu	caa Gln	tca Ser	ggg Gly 475	cat His	ttg Leu	aaa Lys	2343
tgc Cys 480	aga Arg	gct Ala	aag Lys	ctt Leu	gac Asp	aag Lys 485	gtc Val	aaa Lys	atc Ile	aag Lys	gga Gly 490	acg Thr	aca Thr	tat Tyr	ggc Gly	2391
atg Met 495	tgt Cys	gac Asp	tct Ser	gcc Ala	ttc Phe 500	acc Thr	ttc Phe	agc Ser	aag Lys	aac Asn 505	cca Pro	act Thr	gac Asp	aca Thr	ggg Gly 510	2439
cac His	ggg Gly	aca Thr	gtg Val 515	att Ile	gtg Val	gaa Glu	ctg Leu	cag Gln	tat Tyr 520	act Thr	gga Gly	agc Ser	aac Asn	gga Gly 525	ccc Pro	2487
tgc Cys	cga Arg	gtt Val	ccc Pro	atc Ile	tcc Ser	gtg Val	act Thr	gca Ala	aac Asn	ctc Leu	atg Met	gat Asp	ttg Leu	aca Thr	ccg Pro	2535

811252																
530					535					540						
ggt	gga	aga	ttg	gtc	acg	gtc	aat	ccc	ttt	ata	agc	aca	ggg	gga	gcg	2583
Val	Gly	Arg	Leu	Val	Thr	Val	Asn	Pro	Phe	Ile	Ser	Thr	Gly	Gly	Ala	
		545					550					555				
aac	aac	aag	gtc	atg	atc	gaa	gtt	gaa	cca	ccc	ttt	ggc	gat	tct	tac	2631
Asn	Asn	Lys	Val	Met	Ile	Glu	Val	Glu	Pro	Pro	Phe	Gly	Asp	Ser	Tyr	
		560				565					570					
atc	gtc	gtc	gga	aga	ggc	acc	acc	cag	att	aac	tac	cac	tgg	cac	aaa	2679
Ile	Val	Val	Gly	Arg	Gly	Thr	Thr	Gln	Ile	Asn	Tyr	His	Trp	His	Lys	
575					580					585					590	
gag	gga	agc	agc	att	ggg	aag	gct	ttg	gcg	acc	aca	tgg	aaa	gga	gcc	2727
Glu	Gly	Ser	Ser	Ile	Gly	Lys	Ala	Leu	Ala	Thr	Thr	Trp	Lys	Gly	Ala	
				595					600					605		
caa	cgg	cta	gcc	gtc	tta	ggg	gac	aca	gcg	tgg	gac	ttt	gga	tct	att	2775
Gln	Arg	Leu	Ala	Val	Leu	Gly	Asp	Thr	Ala	Trp	Asp	Phe	Gly	Ser	Ile	
			610					615					620			
gga	gga	gtt	ttc	aat	tca	att	ggc	aaa	gct	gtc	cac	caa	gtt	ttc	gga	2823
Gly	Gly	Val	Phe	Asn	Ser	Ile	Gly	Lys	Ala	Val	His	Gln	Val	Phe	Gly	
		625					630					635				
gga	gcg	ttc	agg	act	ctg	ttc	ggg	gga	atg	tcc	tgg	atc	aca	cag	ggg	2871
Gly	Ala	Phe	Arg	Thr	Leu	Phe	Gly	Gly	Met	Ser	Trp	Ile	Thr	Gln	Gly	
	640					645					650					
cta	ctt	gga	gct	ctt	ctc	ctg	tgg	atg	ggg	ttg	cag	gcc	cgc	gac	agg	2919
Leu	Leu	Gly	Ala	Leu	Leu	Leu	Trp	Met	Gly	Leu	Gln	Ala	Arg	Asp	Arg	
655					660				665						670	
agc	atc	tcg	ctg	act	cta	ctg	gct	gtc	gga	ggg	att	ctc	atc	ttt	ctg	2967
Ser	Ile	Ser	Leu	Thr	Leu	Leu	Ala	Val	Gly	Gly	Ile	Leu	Ile	Phe	Leu	
				675					680					685		
gca	acc	agc	gtg	caa	gcc	tgagcggccg	ctcgcagcatg	catctagagg								3015
Ala	Thr	Ser	Val	Gln	Ala											
			690													
gccctattct	atagtgtcac	ctaaatgcta	gagctcgctg	atcagcctcg	actgtgcctt											3075
ctagttgcca	gccatctggt	gtttgcccct	cccccgctgc	ttccttgacc	ctggaagggtg											3135
ccactccac	tgctctttcc	taataaaatg	aggaaattgc	atcgattgt	ctgagtaggt											3195
gtcattctat	tctgggggggt	gggggtgggc	aggacagcaa	gggggaggat	tgggaagaca											3255
atagcaggca	tgctggggat	gcggtgggct	ctatggcttc	tgaggcggaa	agaacagctg											3315
cattaatgaa	tcggccaacg	cgcggggaga	ggcggtttgc	gtattgggcg	ctcttccgct											3375
tcctcgctca	ctgactcgct	gcgctcggtc	gttcggctgc	ggcgagcggt	atcagctcac											3435
tcaaaggcgg	taatacgggt	atccacagaa	tcaggggata	acgcaggaaa	gaacatgtga											3495
gcaaaaggcc	agcaaaaggc	caggaaccgt	aaaaaggccg	cgttgctggc	gtttttccat											3555
aggctccgcc	cccctgacga	gcatcacaaa	aatcgacgct	caagtcagag	gtggcgaaac											3615
ccgacaggac	tataaagata	ccaggcggtt	ccccctggaa	gctccctcgt	gcgctctcct											3675

811252

gttccgaccc	tgccgcttac	cggatacctg	tccgcctttc	tcccttcggg	aagcgtggcg	3735
ctttctcaat	gctcacgctg	taggtatctc	agttcggtgt	aggtcgttcg	ctccaagctg	3795
ggctgtgtgc	acgaaccccc	cgttcagccc	gaccgctgcg	ccttatccgg	taactatcgt	3855
cttgagtcca	acccggttaag	acacgactta	tcgccactgg	cagcagccac	tggtaacagg	3915
attagcagag	cgaggatatgt	aggcgggtgct	acagagttct	tgaagtgggtg	gcctaactac	3975
ggctacacta	gaaggacagt	at ttgggtatc	tgcgctctgc	tgaagccagt	taccttcgga	4035
aaaagagttg	gtagctcttg	atccggcaaa	caaaccaccg	ctggtagcgg	tggttttttt	4095
gtttgcaagc	agcagattac	gcgcagaaaa	aaaggatctc	aagaagatcc	tttgatcttt	4155
tctacggggg	ctgacgctca	gtggaacgaa	aactcacggt	aagggatttt	ggcatgaga	4215
ttatcaaaaa	ggatcttcac	ctagatcctt	ttaaattaaa	aatgaagttt	taaatcaatc	4275
taaagtatat	atgagtaaac	ttgggtctgac	agttaccaat	gcttaatcag	tgaggcacct	4335
atctcagcga	tctgtctatt	tcgttcatcc	atagttgcct	gactccccgt	cgtgtagata	4395
actacgatac	gggaggggctt	accatctggc	cccagtgctg	caatgatacc	gcgagaccca	4455
cgctcaccgg	ctccagattt	atcagcaata	aaccagccag	ccggaagggc	cgagcgcaga	4515
agtggctctg	caactttatc	cgcttccatc	cagtctatta	attgttgccg	ggaagctaga	4575
gtaagtagtt	cgccagttaa	tagtttgcg	aacgttgttg	ccattgctac	aggcatcgtg	4635
gtgtcacgct	cgtcgttttg	tatggcttca	ttcagctccg	gttcccaacg	atcaaggcga	4695
gttacatgat	cccccatggt	gtgcaaaaaa	gcggttagct	ccttcggtcc	tccgatcgtt	4755
gtcagaagta	agttggccgc	agtgttatca	ctcatggtta	tggcagcact	gcataattct	4815
cttactgtca	tgccatccgt	aagatgcttt	tctgtgactg	gtgagtactc	aaccaagtca	4875
ttctgagaat	agtgtatgcg	gcgaccgagt	tgctcttgcc	cggcgtcaat	acgggataat	4935
accgcgccac	atagcagaac	tttaaaagt	ctcatcattg	gaaaacgttc	ttcggggcga	4995
aaactctcaa	ggatcttacc	gctgttgaga	tccagttcga	tgtaaccac	tcgtgcaccc	5055
aactgatctt	cagcatcttt	tactttcacc	agcgtttctg	ggtgagcaaa	aacaggaagg	5115
caaatgccg	caaaaaagg	aataagggcg	acacggaaat	gttgaatact	catactcttc	5175
ctttttcaat	attattgaag	catttatcag	ggttattgtc	tcattgagcg	atacatattt	5235
gaatgtattt	agaaaaataa	acaaataggg	gttccgcgca	catttccccg	aaaagtgcc	5295
cctgacgtc						5304

<210> 22
 <211> 692
 <212> PRT
 <213> Artificial Sequence

811252

<220>

<223> Synthetic Construct

<400> 22

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr Gln Gly
20 25 30

Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala Ile Asn
35 40 45

Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala Leu Asp
50 55 60

Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro Val Leu
65 70 75 80

Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp Val Glu
85 90 95

Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His Ser Arg
100 105 110

Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser Thr Leu
115 120 125

Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr Lys Tyr
130 135 140

Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr Ala Leu
145 150 155 160

Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr Gln Arg
165 170 175

Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr Ser Phe
180 185 190

Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala Ser Gly
195 200 205

Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val Thr Val
210 215 220

Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys Met Glu
225 230 235 240

811252

Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala Thr Leu
245 250 255

Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala His
260 265 270

Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp Val Val
275 280 285

Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile
290 295 300

Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly Lys Thr
305 310 315 320

Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly
325 330 335

Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile Gly Lys
340 345 350

Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser Phe Thr
355 360 365

Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu Ala Arg
370 375 380

Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys Glu Lys
385 390 395 400

Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu Pro Trp
405 410 415

Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu Val Glu
420 425 430

Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu Gly Ser
435 440 445

Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro Ala Thr
450 455 460

Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys Cys Arg
465 470 475 480

Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly Met Cys
Page 43

811252

<220>

<221> CDS

<222> (910)..(2952)

<400> 23

```

gacggatcgg gagatctccc gatccccctat ggtcgactct cagtacaatc tgctctgatg      60
ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg      120
cgagcaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180
ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240
gattattgac tagttattaa tagtaatcaa ttacgggggtc attagttcat agcccatata      300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc      360
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420
attgacgtca atgggtggac tatttacggg aaactgccca cttggcagta catcaagtgt      480
atcatatgcc aagtacgcc cctattgacg tcaatgacgg taaatggccc gcctggcatt      540
atgcccagta catgacctta tgggactttc ctacttgga gtacatctac gtattagtca      600
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg      660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc      720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg      780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaacca      840
ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttggtacc      900
gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc      951
          Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
          1              5              10

ttg gca gtt gtc ata gct ggt aca agc gct gtg acc ttg gtg cgg aaa      999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys
15              20              25              30

aac aga tgg ttg ctc cta aat gtg aca tct gag gac ctc ggg aaa aca      1047
Asn Arg Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr
35              40              45

ttc tct gtg ggc aca ggc aac tgc aca aca aac att ttg gaa gcc aag      1095
Phe Ser Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys
50              55              60

tac tgg tgc cca gac tca atg gaa tac aac tgt ccc aat ctc agt cca      1143
Tyr Trp Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro
65              70              75

aga gag gag cca gat gac att gat tgc tgg tgc tat ggg gtg gaa aac      1191
Arg Glu Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn
80              85              90

gtt aga gtc gca tat ggt aag tgt gac tca gca ggc agg tct agg agg      1239
Val Arg Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg
95              100              105              110

```

tca	aga	agg	gcc	att	gac	ttg	cct	acg	cat	gaa	aac	cat	ggt	ttg	aag	1287
Ser	Arg	Arg	Ala	Ile	Asp	Leu	Pro	Thr	His	Glu	Asn	His	Gly	Leu	Lys	
				115					120					125		
acc	cgg	caa	gaa	aaa	tgg	atg	act	gga	aga	atg	ggt	gaa	agg	caa	ctc	1335
Thr	Arg	Gln	Glu	Lys	Trp	Met	Thr	Gly	Arg	Met	Gly	Glu	Arg	Gln	Leu	
			130					135					140			
caa	aag	att	gag	aga	tgg	ttc	gtg	agg	aac	ccc	ttt	ttt	gca	gtg	acg	1383
Gln	Lys	Ile	Glu	Arg	Trp	Phe	Val	Arg	Asn	Pro	Phe	Phe	Ala	Val	Thr	
		145					150					155				
gct	ctg	acc	att	gcc	tac	ctt	gtg	gga	agc	aac	atg	acg	caa	cga	gtc	1431
Ala	Leu	Thr	Ile	Ala	Tyr	Leu	Val	Gly	Ser	Asn	Met	Thr	Gln	Arg	Val	
	160					165					170					
gtg	att	gcc	cta	ctg	gtc	ttg	gct	gtt	ggt	ccg	gcc	tac	tca	gct	cac	1479
Val	Ile	Ala	Leu	Leu	Val	Leu	Ala	Val	Gly	Pro	Ala	Tyr	Ser	Ala	His	
					180					185					190	
tgc	att	gga	att	act	gac	agg	gat	ttc	att	gag	ggg	gtg	cat	gga	gga	1527
Cys	Ile	Gly	Ile	Thr	Asp	Arg	Asp	Phe	Ile	Glu	Gly	Val	His	Gly	Gly	
				195					200					205		
act	tgg	gtt	tca	gct	acc	ctg	gag	caa	gac	aag	tgt	gtc	act	gtt	atg	1575
Thr	Trp	Val	Ser	Ala	Thr	Leu	Glu	Gln	Asp	Lys	Cys	Val	Thr	Val	Met	
			210					215					220			
gcc	cct	gac	aag	cct	tca	ttg	gac	atc	tca	cta	gag	aca	gta	gcc	att	1623
Ala	Pro	Asp	Lys	Pro	Ser	Leu	Asp	Ile	Ser	Leu	Glu	Thr	Val	Ala	Ile	
		225					230					235				
gat	aga	cct	gct	gag	gtg	agg	aaa	gtg	tgt	tac	aat	gca	gtt	ctc	act	1671
Asp	Arg	Pro	Ala	Glu	Val	Arg	Lys	Val	Cys	Tyr	Asn	Ala	Val	Leu	Thr	
	240					245					250					
cat	gtg	aag	att	aat	gac	aag	tgc	ccc	agc	act	gga	gag	gcc	cac	cta	1719
His	Val	Lys	Ile	Asn	Asp	Lys	Cys	Pro	Ser	Thr	Gly	Glu	Ala	His	Leu	
				260						265					270	
gct	gaa	gag	aac	gaa	ggg	gac	aat	gcg	tgc	aag	cgc	act	tat	tct	gat	1767
Ala	Glu	Glu	Asn	Glu	Gly	Asp	Asn	Ala	Cys	Lys	Arg	Thr	Tyr	Ser	Asp	
				275					280					285		
aga	ggc	tgg	ggc	aat	ggc	tgt	ggc	cta	ttt	ggg	aaa	ggg	agc	att	gtg	1815
Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile	Val	
			290					295					300			
gca	tgc	gcc	aaa	ttc	act	tgt	gcc	aaa	tcc	atg	agt	ttg	ttt	gag	gtt	1863
Ala	Cys	Ala	Lys	Phe	Thr	Cys	Ala	Lys	Ser	Met	Ser	Leu	Phe	Glu	Val	
		305					310					315				
gat	cag	acc	aaa	att	cag	tat	gtc	atc	aga	gca	caa	ttg	cat	gta	ggg	1911
Asp	Gln	Thr	Lys	Ile	Gln	Tyr	Val	Ile	Arg	Ala	Gln	Leu	His	Val	Gly	
		320				325					330					
gcc	aag	cag	gaa	aat	tgg	act	acc	gac	att	aag	act	ctc	aag	ttt	gat	1959
Ala	Lys	Gln	Glu	Asn	Trp	Thr	Thr	Asp	Ile	Lys	Thr	Leu	Lys	Phe	Asp	
					340					345					350	
gcc	ctg	tca	ggc	tcc	cag	gaa	gtc	gag	ttc	att	ggg	tat	gga	aaa	gct	2007
Ala	Leu	Ser	Gly	Ser	Gln	Glu	Val	Glu	Phe	Ile	Gly	Tyr	Gly	Lys	Ala	

															811252	
Asp	Phe	Ser	Ser	Ala	Gly	Gly	Phe	Phe	Thr	Ser	Val	Gly	Lys	Gly	Ile	
			610					615					620			
cat	acg	gtg	ttt	ggc	tct	gcc	ttt	cag	ggg	cta	ttt	ggc	ggc	ttg	aac	2823
His	Thr	Val	Phe	Gly	Ser	Ala	Phe	Gln	Gly	Leu	Phe	Gly	Gly	Leu	Asn	
		625					630					635				
tgg	ata	aca	aag	gtc	atc	atg	ggg	gcg	gta	ctt	ata	tgg	ggt	ggc	atc	2871
Trp	Ile	Thr	Lys	Val	Ile	Met	Gly	Ala	Val	Leu	Ile	Trp	Val	Gly	Ile	
		640				645					650					
aac	aca	aga	aac	atg	aca	atg	tcc	atg	agc	atg	atc	ttg	gta	gga	gtg	2919
Asn	Thr	Arg	Asn	Met	Thr	Met	Ser	Met	Ser	Met	Ile	Leu	Val	Gly	Val	
		655			660				665						670	
atc	atg	atg	ttt	ttg	tct	cta	gga	ggt	ggg	gcg	tgagcggccg	ctc	gagcatg			2972
Ile	Met	Met	Phe	Leu	Ser	Leu	Gly	Val	Gly	Ala						
			675						680							
catctagagg	gccctattct	atagtgtcac	ctaaatgcta	gagctcgctg	atcagcctcg											3032
actgtgcctt	ctagttgccca	gccatctgtt	gtttgcccct	ccccctgcc	ttccttgacc											3092
ctggaagggtg	ccactcccac	tgtcctttcc	taataaaatg	aggaaattgc	atcgcatgtg											3152
ctgagtaggt	gtcattctat	tctggggggt	gggggtggggc	aggacagcaa	gggggaggat											3212
tggaagaca	atagcaggca	tgctggggat	gcggtgggct	ctatggcttc	tgaggcggaa											3272
agaacagctg	cattaatgaa	tcggccaacg	gcgggggaga	ggcggtttgc	gtattgggcg											3332
ctcttccgct	tcctcgctca	ctgactcgct	gcgctcggtc	gttcggctgc	ggcgagcggt											3392
atcagctcac	tcaaaggcgg	taatacgggt	atccacagaa	tcaggggata	acgcaggaaa											3452
gaacatgtga	gcaaaaggcc	agcaaaaggc	caggaaccgt	aaaaaggccg	cgttgctggc											3512
gtttttccat	aggctccgcc	cccctgacga	gcatcacaaa	aatcgacgct	caagtcagag											3572
gtggcgaaac	ccgacaggac	tataaagata	ccaggcgttt	ccccctggaa	gctccctcgt											3632
gcgctctcct	gttccgaccc	tgccgcttac	cggatacctg	tccgcctttc	tcccttcggg											3692
aagcgtggcg	ctttctcaat	gtcacgctg	taggtatctc	agttcggtgt	aggtcgttcg											3752
ctccaagctg	ggctgtgtgc	acgaaccccc	cgttcagccc	gaccgctgcg	ccttatccgg											3812
taactatcgt	cttgagtcca	accggttaag	acacgactta	tcgccactgg	cagcagccac											3872
tggtaacagg	attagcagag	cgaggatatgt	aggcgggtgct	acagagttct	tgaagtgggtg											3932
gcctaactac	ggctacacta	gaaggacagt	atgttggtatc	tgcgctctgc	tgaagccagt											3992
taccttcgga	aaaagagttg	gtagctcttg	atccggcaaa	caaaccaccg	ctggtagcgg											4052
tggttttttt	gtttgcaagc	agcagattac	gcgcagaaaa	aaaggatctc	aagaagatcc											4112
tttgatcttt	tctacggggt	ctgacgtca	gtggaacgaa	aactcacgtt	aagggatttt											4172
ggtcatgaga	ttatcaaaaa	ggatcttcac	ctagatcctt	ttaaattaaa	aatgaagttt											4232
taaatcaatc	taaagtatat	atgagtaaac	ttgggtctgac	agttaccaat	gcttaatcag											4292

811252

```

tgaggcacct atctcagcga tctgtctatt tcgttcatcc atagttgcct gactccccgt 4352
cgtgtagata actacgatac gggagggcctt accatctggc cccagtgtg caatgatacc 4412
gcgagaccca cgctcaccgg ctccagattt atcagcaata aaccagccag ccggaagggc 4472
cgagcgcaga agtggctctg caactttatc cgcctccatc cagtctatta attgttgccg 4532
ggaagctaga gtaagtagtt cgccagttaa tagtttgcg aacgttggtg ccattgctac 4592
aggcatcgtg gtgtcacgct cgtcgtttgg tatggcttca ttcagctccg gttcccaacg 4652
atcaaggcga gttacatgat ccccatgtt gtgcaaaaaa gcggttagct ccttcggtcc 4712
tccgatcgtt gtcagaagta agttggccgc agtgttatca ctcatggtta tggcagcact 4772
gcataattct cttactgtca tgccatccgt aagatgcttt tctgtgactg gtgagtactc 4832
aaccaagtca ttctgagaat agtgatgcg gcgaccgagt tgctcttgcc cggcgtaaat 4892
acgggataat accgcgccac atagcagaac tttaaaagtg ctcatcattg gaaaacgttc 4952
ttcggggcga aaactctcaa ggatcttacc gctgttgaga tccagttcga tgtaaccac 5012
tcgtgcaccc aactgatctt cagcatcttt tactttcacc agcgtttctg ggtgagcaaa 5072
aacaggaagg caaatgccg caaaaaagg aataagggcg acacggaaat gttgaatact 5132
catactcttc ctttttcaat attattgaag catttatcag ggttattgtc tcatgagcgg 5192
atacatattt gaatgtattt agaaaaataa acaaataggg gttccgcgca catttccccg 5252
aaaagtgcc cctgacgtc 5271

```

<210> 24
 <211> 681
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 24

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
 1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys Asn Arg
 20 25 30

Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr Phe Ser
 35 40 45

Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys Tyr Trp
 50 55 60

Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro Arg Glu
 65 70 75 80

811252

Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn Val Arg
85 90 95

Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg Ser Arg
100 105 110

Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys Thr Arg
115 120 125

Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu Gln Lys
130 135 140

Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr Ala Leu
145 150 155 160

Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val Val Ile
165 170 175

Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His Cys Ile
180 185 190

Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly Thr Trp
195 200 205

Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met Ala Pro
210 215 220

Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile Asp Arg
225 230 235 240

Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr His Val
245 250 255

Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu Ala Glu
260 265 270

Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp Arg Gly
275 280 285

Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val Ala Cys
290 295 300

Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val Asp Gln
305 310 315 320

Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly Ala Lys

811252

325	330	335
Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp Ala Leu		
340	345	350
Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala Thr Leu		
355	360	365
Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr Ile Ala		
370	375	380
Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala Gln Asp		
385	390	395
Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg Glu Met		
405	410	415
His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile Arg Val		
420	425	430
Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly		
435	440	445
Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu		
450	455	460
His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu		
465	470	475
Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys		
485	490	495
Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val		
500	505	510
Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu		
515	520	525
Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala		
530	535	540
Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly		
545	550	555
Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln		
565	570	575

811252

Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met
580 585 590

Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe
595 600 605

Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr
610 615 620

Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile
625 630 635 640

Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr
645 650 655

Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met
660 665 670

Met Phe Leu Ser Leu Gly Val Gly Ala
675 680

<210> 25
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<222> (1)..(35)
<223> POW 454

<400> 25
aaaagaaaaa gcgctaccac catccaccgg gacag 35

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<222> (1)..(41)
<223> CPOW 2417

<400> 26
actgttacc tcaaccccg actcgccggc gaaaaagaaa a 41

811252

<210> 27
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<223> Modified JE Signal

<400> 27

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala
20

<210> 28
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<222> (1)..(36)
<223> YF 482

<400> 28
aaaagaaaaa gcgctgtgac cttggtgcgg aaaaac 36

<210> 29
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<222> (1)..(41)
<223> CYF 2433

<400> 29
acagagatcc tcaaccccgcc actcgccggc gaaaaagaaa a 41

<210> 30
<211> 41
<212> DNA

811252

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> misc_feature

<222> (1)..(41)

<223> SLE 463

<400> 30

aaaagaaaaa gcgctttgca gttatcaacc tatcagggga a 41

<210> 31

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> misc_feature

<222> (1)..(40)

<223> CSLE 2477

<400> 31

accgttggtc gcacgttcgg actcgccggc gaaaaagaaa 40

<210> 32

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 32

Leu Asp Thr Ile Asn Arg Arg Pro Ser Lys Lys Arg Gly Gly Thr Arg
1 5 10 15

Ser Leu Leu Gly Leu Ala Ala Leu Ile Gly Leu Ala Ser Ser Leu Gln
20 25 30

Leu Leu Ser Thr Tyr Gln Gly
35

<210> 33

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

811252

<400> 33

Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met
1 5 10 15

Lys Leu Ser Asn Phe Gln Gly Lys
20

<210> 34

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 34

Met Asn Glu Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile
1 5 10 15

Ala Cys Ala Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys
20 25 30

<210> 35

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 35

Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met
1 5 10 15

Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys
20 25 30

Leu Ser Asn Phe Gln Gly Lys
35

<210> 36

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 36

Met Ser Lys Lys Arg Gly Gly Ser Glu Thr Ser Val Leu Met Val Ile
1 5 10 15

811252

Phe Met Leu Ile Gly Phe Ala Ala Ala Leu Lys Leu Ser Asn Phe Gln
20 25 30

Gly Lys

<210> 37
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct
<400> 37

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn Phe Gln Gly
20 25 30

Lys

<210> 38
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct
<400> 38

Met Asn Val Leu Arg Gly Phe Arg Lys Glu Ile Gly Arg Met Leu Asn
1 5 10 15

Ile Leu Asn Arg Arg Arg Arg Thr Ala Gly Met Ile Ile Met Leu Ile
20 25 30

Pro Thr Val Met Ala Phe His Leu Thr Thr Arg Asn Gly Glu
35 40 45

<210> 39
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct
<400> 39

811252

Met Val Gly Leu Gln Lys Arg Gly Lys Arg Arg Ser Ala Thr Asp Trp
1 5 10 15

Met Ser Trp Leu Leu Val Ile Thr Leu Leu Gly Met Thr Leu Ala Ala
20 25 30

Thr Val Arg Lys Glu Arg Gly Asp
35 40

<210> 40
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct
<400> 40

Met Gly Trp Leu Leu Val Val Val Leu Leu Gly Val Thr Leu Ala Ala
1 5 10 15

Thr Val Arg Lys Glu Arg Gly Asp
20

<210> 41
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct
<400> 41

Met Ser Trp Leu Leu Val Ile Thr Leu Leu Gly Met Thr Ile Ala Ala
1 5 10 15

Thr Val Arg Lys Glu Arg Gly Asp
20

<210> 42
<211> 5292
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> CDS
<222> (910)..(2964)

<400> 42
gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctgatg 60
Page 57

ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg	120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc	180
ttagggtag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt	240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata	300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc	360
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc	420
attgacgtca atgggtggag tattttacggg aaactgcccc cttggcagta catcaagtgt	480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt	540
atgccagta catgacctta tgggactttc ctacttgga gtacatctac gtattagtca	600
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg	660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc	720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc ccattgacg caaatgggcg	780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaacca	840
ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttggtacc	900
gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc	951
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser	
1 5 10	
ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt	999
Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg	
15 20 25 30	
aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt	1047
Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser	
35 40 45	
ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc	1095
Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala	
50 55 60	
atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc	1143
Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro	
65 70 75	
ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct	1191
Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser	
80 85 90	
acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat	1239
Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His	
95 100 105 110	
aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga	1287
Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly	
115 120 125	
ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa	1335
Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys	

811252																
130					135					140						
cat	gtc	cag	aga	att	gaa	act	tgg	atc	ttg	aga	cat	cca	ggc	ttc	acc	1383
His	Val	Gln	Arg	Ile	Glu	Thr	Trp	Ile	Leu	Arg	His	Pro	Gly	Phe	Thr	
		145					150					155				
atg	atg	gca	gca	atc	ctg	gca	tac	acc	ata	gga	acg	aca	cat	ttc	caa	1431
Met	Met	Ala	Ala	Ile	Leu	Ala	Tyr	Thr	Ile	Gly	Thr	Thr	His	Phe	Gln	
		160				165					170					
aga	gcc	ctg	att	ttc	atc	tta	ctg	aca	gct	gtc	act	cct	tca	atg	aca	1479
Arg	Ala	Leu	Ile	Phe	Ile	Leu	Leu	Thr	Ala	Val	Thr	Pro	Ser	Met	Thr	
175					180					185					190	
atg	cgt	tgc	ata	gga	atg	tca	aat	aga	gac	ttt	gtg	gaa	ggg	gtt	tca	1527
Met	Arg	Cys	Ile	Gly	Met	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Val	Ser	
				195					200					205		
gga	gga	agc	tgg	gtt	gac	ata	gtc	tta	gaa	cat	gga	agc	tgt	gtg	acg	1575
Gly	Gly	Ser	Trp	Val	Asp	Ile	Val	Leu	Glu	His	Gly	Ser	Cys	Val	Thr	
			210					215					220			
acg	atg	gca	aaa	aac	aaa	cca	aca	ttg	gat	ttt	gaa	ctg	ata	aaa	aca	1623
Thr	Met	Ala	Lys	Asn	Lys	Pro	Thr	Leu	Asp	Phe	Glu	Leu	Ile	Lys	Thr	
		225					230					235				
gaa	gcc	aaa	cag	cct	gcc	acc	cta	agg	aag	tac	tgt	ata	gag	gca	aag	1671
Glu	Ala	Lys	Gln	Pro	Ala	Thr	Leu	Arg	Lys	Tyr	Cys	Ile	Glu	Ala	Lys	
	240					245					250					
cta	acc	aac	aca	aca	aca	gaa	tct	cgc	tgc	cca	aca	caa	ggg	gaa	ccc	1719
Leu	Thr	Asn	Thr	Thr	Thr	Glu	Ser	Arg	Cys	Pro	Thr	Gln	Gly	Glu	Pro	
					260					265					270	
agc	cta	aat	gaa	gag	cag	gac	aaa	agg	ttc	gtc	tgc	aaa	cac	tcc	atg	1767
Ser	Leu	Asn	Glu	Glu	Gln	Asp	Lys	Arg	Phe	Val	Cys	Lys	His	Ser	Met	
				275					280					285		
gta	gac	aga	gga	tgg	gga	aat	gga	tgt	gga	cta	ttt	gga	aag	gga	ggc	1815
Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Gly	
			290					295					300			
att	gtg	acc	tgt	gct	atg	ttc	aga	tgc	aaa	aag	aac	atg	gaa	gga	aaa	1863
Ile	Val	Thr	Cys	Ala	Met	Phe	Arg	Cys	Lys	Lys	Asn	Met	Glu	Gly	Lys	
		305					310					315				
gtt	gtg	caa	cca	gaa	aac	ttg	gaa	tac	acc	att	gtg	ata	aca	cct	cac	1911
Val	Val	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Thr	Ile	Val	Ile	Thr	Pro	His	
		320				325					330					
tca	ggg	gaa	gag	cat	gca	gtc	gga	aat	gac	aca	gga	aaa	cat	ggc	aag	1959
Ser	Gly	Glu	Glu	His	Ala	Val	Gly	Asn	Asp	Thr	Gly	Lys	His	Gly	Lys	
					340					345					350	
gaa	atc	aaa	ata	aca	cca	cag	agt	tcc	atc	aca	gaa	gca	gaa	ttg	aca	2007
Glu	Ile	Lys	Ile	Thr	Pro	Gln	Ser	Ser	Ile	Thr	Glu	Ala	Glu	Leu	Thr	
				355					360					365		
ggt	tat	ggc	act	gtc	aca	atg	gag	tgc	tct	cca	aga	acg	ggc	ctc	gac	2055
Gly	Tyr	Gly	Thr	Val	Thr	Met	Glu	Cys	Ser	Pro	Arg	Thr	Gly	Leu	Asp	
			370					375					380			
ttc	aat	gag	atg	gtg	ttg	ttg	cag	atg	gaa	aat	aaa	gct	tgg	ctg	gtg	2103

																811252	
Phe	Asn	Glu	Met	Val	Leu	Leu	Gln	Met	Glu	Asn	Lys	Ala	Trp	Leu	Val		
		385					390					395					
cac	agg	caa	tgg	ttc	cta	gac	ctg	ccg	tta	cca	tgg	ttg	ccc	gga	gcg	2151	
His	Arg	Gln	Trp	Phe	Leu	Asp	Leu	Pro	Leu	Pro	Trp	Leu	Pro	Gly	Ala		
		400					405					410					
gac	aca	caa	ggg	tca	aat	tgg	ata	cag	aaa	gag	aca	ttg	gtc	act	ttc	2199	
Asp	Thr	Gln	Gly	Ser	Asn	Trp	Ile	Gln	Lys	Glu	Thr	Leu	Val	Thr	Phe		
		415					420					425				430	
aaa	aat	ccc	cat	gcg	aag	aaa	cag	gat	ggt	ggt	ggt	tta	gga	tcc	caa	2247	
Lys	Asn	Pro	His	Ala	Lys	Lys	Gln	Asp	Val	Val	Val	Leu	Gly	Ser	Gln		
							435					440			445		
gaa	ggg	gcc	atg	cac	aca	gca	ctt	aca	ggg	gcc	aca	gaa	atc	caa	atg	2295	
Glu	Gly	Ala	Met	His	Thr	Ala	Leu	Thr	Gly	Ala	Thr	Glu	Ile	Gln	Met		
							450					455			460		
tca	tca	gga	aac	tta	ctc	ttc	aca	gga	cat	ctc	aag	tgc	agg	ctg	aga	2343	
Ser	Ser	Gly	Asn	Leu	Leu	Phe	Thr	Gly	His	Leu	Lys	Cys	Arg	Leu	Arg		
		465					470					475					
atg	gac	aag	cta	cag	ctc	aaa	gga	atg	tca	tac	tct	atg	tgc	aca	gga	2391	
Met	Asp	Lys	Leu	Gln	Leu	Lys	Gly	Met	Ser	Tyr	Ser	Met	Cys	Thr	Gly		
		480					485					490					
aag	ttt	aaa	gtt	gtg	aag	gaa	ata	gca	gaa	aca	caa	cat	gga	aca	ata	2439	
Lys	Phe	Lys	Val	Val	Lys	Glu	Ile	Ala	Glu	Thr	Gln	His	Gly	Thr	Ile		
		495					500					505				510	
gtt	atc	aga	gtg	caa	tat	gaa	ggg	gac	ggc	tct	cca	tgc	aag	atc	cct	2487	
Val	Ile	Arg	Val	Gln	Tyr	Glu	Gly	Asp	Gly	Ser	Pro	Cys	Lys	Ile	Pro		
							515					520			525		
ttt	gag	ata	atg	gat	ttg	gaa	aaa	aga	cat	gtc	tta	ggt	cgc	ctg	att	2535	
Phe	Glu	Ile	Met	Asp	Leu	Glu	Lys	Arg	His	Val	Leu	Gly	Arg	Leu	Ile		
							530					535			540		
aca	gtc	aac	cca	att	gtg	aca	gaa	aaa	gat	agc	cca	gtc	aac	ata	gaa	2583	
Thr	Val	Asn	Pro	Ile	Val	Thr	Glu	Lys	Asp	Ser	Pro	Val	Asn	Ile	Glu		
		545					550					555					
gca	gaa	cct	cca	ttc	gga	gac	agc	tac	atc	atc	ata	gga	gta	gag	ccg	2631	
Ala	Glu	Pro	Pro	Phe	Gly	Asp	Ser	Tyr	Ile	Ile	Ile	Gly	Val	Glu	Pro		
		560					565					570					
gga	caa	ctg	aag	ctc	aac	tgg	ttt	aag	aaa	gga	agt	tct	atc	ggc	caa	2679	
Gly	Gln	Leu	Lys	Leu	Asn	Trp	Phe	Lys	Lys	Gly	Ser	Ser	Ile	Gly	Gln		
		575					580					585				590	
atg	ttt	gag	aca	aca	atg	agg	ggg	gcg	aag	aga	atg	gcc	att	tta	ggt	2727	
Met	Phe	Glu	Thr	Thr	Met	Arg	Gly	Ala	Lys	Arg	Met	Ala	Ile	Leu	Gly		
							595					600			605		
gac	aca	gcc	tgg	gat	ttt	gga	tcc	ttg	gga	gga	gtg	ttt	aca	tct	ata	2775	
Asp	Thr	Ala	Trp	Asp	Phe	Gly	Ser	Leu	Gly	Gly	Val	Phe	Thr	Ser	Ile		
							610					615			620		
gga	aag	gct	ctc	cac	caa	gtc	ttt	gga	gca	atc	tat	gga	gct	gcc	ttc	2823	
Gly	Lys	Ala	Leu	His	Gln	Val	Phe	Gly	Ala	Ile	Tyr	Gly	Ala	Ala	Phe		
		625					630					635					

811252

agt ggg gtt tca tgg act atg aaa atc ctc ata gga gtc att atc aca	2871
Ser Gly Val Ser Trp Thr Met Lys Ile Leu Ile Gly Val Ile Ile Thr	
640 645 650	
tgg ata gga atg aat tca cgc agc acc tca ctg tct gtg aca cta gta	2919
Trp Ile Gly Met Asn Ser Arg Ser Thr Ser Leu Ser Val Thr Leu Val	
655 660 665 670	
ttg gtg gga att gtg aca ctg tat ttg gga gtc atg gtg cag gcc	2964
Leu Val Gly Ile Val Thr Leu Tyr Leu Gly Val Met Val Gln Ala	
675 680 685	
taattagttg agcggccgct cgagcatgca tctagagggc cctattctat agtgtcacct	3024
aaatgctaga gctcgtgat cagcctcgac tgtgccttct agttgccagc catctgttgt	3084
ttgccccctcc cccgtgcctt ccttgaccct ggaaggtgcc actcccaactg tcctttccta	3144
ataaaatgag gaaattgcat cgcattgtct gagtaggtgt cattctattc tgggggggtgg	3204
ggtggggcag gacagcaagg gggaggattg ggaagacaat agcaggcatg ctggggatgc	3264
ggtgggctct atggcttctg aggcggaaag aaccagctgc attaatgaat cggccaacgc	3324
gcggggagag gcggtttgcg tattgggcgc tcttcgcctt cctcgctcac tgactcgctg	3384
cgctcggtcg ttcggctgcg gcgagcggtg tcagctcact caaaggcggg aatacggtta	3444
tccacagaat caggggataa cgcaggaaag aacatgtgag caaaaggcca gcaaaaggcc	3504
aggaaccgta aaaaggccgc gttgctggcg tttttccata ggctccgccc ccctgacgag	3564
catcacaaaa atcgacgctc aagtcagagg tggcgaaacc cgacaggact ataaagatac	3624
caggcgtttc cccctggaag ctccctcgtg cgctctcctg ttccgaccct gccgcttacc	3684
ggatacctgt ccgcctttct cccttcggga agcgtggcgc tttctcatag ctacgctgt	3744
aggtatctca gttcgggtgta ggtcgttcgc tccaagctgg gctgtgtgca cgaaccccc	3804
gttcagcccc accgctgcgc cttatccggt aactatcgtc ttgagtccaa cccggtaaga	3864
cacgacttat cgccactggc agcagccact ggtaacagga ttagcagagc gaggtatgta	3924
ggcggtgcta cagagttctt gaagtgtgg cctaactacg gctacactag aagaacagta	3984
tttggtatct gcgctctgct gaagccagtt accttcggaa aaagagttgg tagctcttga	4044
tccggcaaac aaaccaccgc tggtagcggg ggtttttttg ttgcaagca gcagattacg	4104
cgcagaaaaa aaggatctca agaagatcct ttgatctttt ctacggggtc tgacgctcag	4164
tggaacgaaa actcacgtta agggattttg gtcatgagat tatcaaaaag gatcttcacc	4224
tagatccttt taaattaaaa atgaagtttt aaatcaatct aaagtatata tgagtaaact	4284
tggctctgaca gttaccaatg cttaatcagt gaggcaccta tctcagcgat ctgtctattt	4344
cgttcatcca tagttgcctg actccccgtc gtgtagataa ctacgatacg ggagggctta	4404
ccatctggcc ccagtgtgc aatgataccg cgagaccac gtcaccggc tccagattta	4464
tcagcaataa accagccagc cggaaggggc gagcgcagaa gtggtcctgc aactttatcc	4524

811252

gcctccatcc agtctattaa ttgttgccgg gaagctagag taagtagttc gccagttaat 4584
agtttgcgca acgttggtgc cattgctaca ggcacgtgg tgtcacgctc gtcgtttggt 4644
atggcttcat tcagctccgg ttcccaacga tcaaggcgag ttacatgac ccccatgttg 4704
tgcaaaaaag cggttagctc cttcggtcct ccgatcggtg tcagaagtaa gttggccgca 4764
gtgttatcac tcatggttat ggcagcactg cataattctc ttactgtcat gccatccgta 4824
agatgctttt ctgtgactgg tgagtactca accaagtcac tctgagaata gtgtatgcgg 4884
cgaccgagtt gctcttgccc ggcgtcaata cgggataata ccgcgccaca tagcagaact 4944
ttaaaagtc tcatcattgg aaaacgttct tcggggcgaa aactctcaag gatcttaccg 5004
ctgttgagat ccagttcgat gtaaccact cgtgcacca actgatcttc agcatctttt 5064
actttcacca gcgtttctgg gtgagcaaaa acaggaaggc aaaatgccgc aaaaaagggg 5124
ataagggcga cacggaaatg ttgaatactc atactcttcc tttttcaata ttattgaagc 5184
atttatcagg gttattgtct catgagcgga tacatatgtg aatgtattta gaaaaataaa 5244
caaatagggg ttccgcgcac atttccccga aaagtgccac ctgacgtc 5292

<210> 43
<211> 685
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 43

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly
20 25 30

Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
35 40 45

Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
50 55 60

Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
65 70 75 80

Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
85 90 95

Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg
Page 62

811252

100		105		110
Glu Lys Arg Ser Val Ala Leu Val	Pro His Val Gly Met Gly Leu Glu			
115	120	125		
Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val				
130	135	140		
Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met				
145	150	155	160	
Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala				
165	170	175		
Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg				
180	185	190		
Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly				
195	200	205		
Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met				
210	215	220		
Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala				
225	230	235	240	
Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr				
245	250	255		
Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu				
260	265	270		
Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp				
275	280	285		
Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val				
290	295	300		
Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val				
305	310	315	320	
Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly				
325	330	335		
Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile				
340	345	350		

811252

Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr
355 360 365

Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn
370 375 380

Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg
385 390 395 400

Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr
405 410 415

Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn
420 425 430

Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly
435 440 445

Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser
450 455 460

Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp
465 470 475 480

Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe
485 490 495

Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile
500 505 510

Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu
515 520 525

Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val
530 535 540

Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu
545 550 555 560

Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro Gly Gln
565 570 575

Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln Met Phe
580 585 590

Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly Asp Thr
595 600 605

811252

Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile Gly Lys
610 615 620

Ala Leu His Gln Val Phe Gly Ala Ile Tyr Gly Ala Ala Phe Ser Gly
625 630 635 640

Val Ser Trp Thr Met Lys Ile Leu Ile Gly Val Ile Ile Thr Trp Ile
645 650 655

Gly Met Asn Ser Arg Ser Thr Ser Leu Ser Val Thr Leu Val Leu Val
660 665 670

Gly Ile Val Thr Leu Tyr Leu Gly Val Met Val Gln Ala
675 680 685

<210> 44

<211> 5293

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> CDS

<222> (910)..(2964)

<400> 44

gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctgatg	60
ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg	120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc	180
ttagggttag gcgtttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt	240
gattattgac tagttattaa tagtaatcaa ttacgggggtc attagttcat agcccatata	300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc	360
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc	420
attgacgtca atgggtggag tatttacggg aaactgccca cttggcagta catcaagtgt	480
atcatatgcc aagtagcccc cctattgacg tcaatgacgg taaatggccc gcctggcatt	540
atgccagta catgacctta tgggactttc ctacttgga gtacatctac gtattagtca	600
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg	660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc	720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc ccattgacg caaatgggcg	780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccga	840

811252

ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttgggtacc	900
gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser 1 5 10	951
ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg 15 20 25 30	999
aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser 35 40 45	1047
ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala 50 55 60	1095
atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro 65 70 75	1143
ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser 80 85 90	1191
acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His 95 100 105 110	1239
aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly 115 120 125	1287
ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys 130 135 140	1335
cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr 145 150 155	1383
atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln 160 165 170	1431
aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr 175 180 185 190	1479
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser 195 200 205	1527
gga gga agc tgg gtt gac ata gtc tta gaa cat gga agc tgt gtg acg Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr 210 215 220	1575
acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Ile Lys Thr 225 230 235	1623
gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag	1671

															811252	
Glu	Ala	Lys	Gln	Pro	Ala	Thr	Leu	Arg	Lys	Tyr	Cys	Ile	Glu	Ala	Lys	
240						245					250					
cta	acc	aac	aca	aca	aca	gaa	tct	cg	tgc	cca	aca	caa	ggg	gaa	ccc	1719
Leu	Thr	Asn	Thr	Thr	Thr	Glu	Ser	Arg	Cys	Pro	Thr	Gln	Gly	Glu	Pro	
255					260					265					270	
agc	cta	aat	gaa	gag	cag	gac	aaa	agg	ttc	gtc	tgc	aaa	cac	tcc	atg	1767
Ser	Leu	Asn	Glu	Glu	Gln	Asp	Lys	Arg	Phe	Val	Cys	Lys	His	Ser	Met	
			275						280					285		
gta	gac	aga	gga	tgg	gga	aat	gga	tgt	gga	cta	ttt	gga	aag	gga	ggc	1815
Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Gly	
			290					295					300			
att	gtg	acc	tgt	gct	atg	ttc	aga	tgc	aaa	aag	aac	atg	gaa	gga	aaa	1863
Ile	Val	Thr	Cys	Ala	Met	Phe	Arg	Cys	Lys	Lys	Asn	Met	Glu	Gly	Lys	
		305					310					315				
gtt	gtg	caa	cca	gaa	aac	ttg	gaa	tac	acc	att	gtg	ata	aca	cct	cac	1911
Val	Val	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Thr	Ile	Val	Ile	Thr	Pro	His	
	320					325					330					
tca	ggg	gaa	gag	cat	gca	gtc	gga	aat	gac	aca	gga	aaa	cat	ggc	aag	1959
Ser	Gly	Glu	Glu	His	Ala	Val	Gly	Asn	Asp	Thr	Gly	Lys	His	Gly	Lys	
335					340					345					350	
gaa	atc	aaa	ata	aca	cca	cag	agt	tcc	atc	aca	gaa	gca	gaa	ttg	aca	2007
Glu	Ile	Lys	Ile	Thr	Pro	Gln	Ser	Ser	Ile	Thr	Glu	Ala	Glu	Leu	Thr	
				355					360					365		
ggt	tat	ggc	act	gtc	aca	atg	gag	tgc	tct	cca	aga	acg	ggc	ctc	gac	2055
Gly	Tyr	Gly	Thr	Val	Thr	Met	Glu	Cys	Ser	Pro	Arg	Thr	Gly	Leu	Asp	
			370					375					380			
ttc	aat	gag	atg	gtg	ttg	ttg	cag	atg	gaa	aat	aaa	gct	tgg	ctg	gtg	2103
Phe	Asn	Glu	Met	Val	Leu	Leu	Gln	Met	Glu	Asn	Lys	Ala	Trp	Leu	Val	
		385					390					395				
cac	agg	caa	tgg	ttc	cta	gac	ctg	ccg	tta	cca	tgg	ttg	ccc	gga	gcg	2151
His	Arg	Gln	Trp	Phe	Leu	Asp	Leu	Pro	Leu	Pro	Trp	Leu	Pro	Gly	Ala	
	400					405					410					
gac	aca	caa	ggg	tca	aat	tgg	ata	cag	aaa	gag	aca	ttg	gtc	act	ttc	2199
Asp	Thr	Gln	Gly	Ser	Asn	Trp	Ile	Gln	Lys	Glu	Thr	Leu	Val	Thr	Phe	
415					420					425					430	
aaa	aat	ccc	cat	gcg	aag	aaa	cag	gat	ggt	ggt	ggt	tta	gga	tcc	caa	2247
Lys	Asn	Pro	His	Ala	Lys	Lys	Gln	Asp	Val	Val	Val	Leu	Gly	Ser	Gln	
				435					440					445		
gaa	ggg	gcc	atg	cac	aca	gca	ctt	aca	ggg	gcc	aca	gaa	atc	caa	atg	2295
Glu	Gly	Ala	Met	His	Thr	Ala	Leu	Thr	Gly	Ala	Thr	Glu	Ile	Gln	Met	
			450					455					460			
tca	tca	gga	aac	tta	ctc	ttc	aca	gga	cat	ctc	aag	tgc	agg	ctg	aga	2343
Ser	Ser	Gly	Asn	Leu	Leu	Phe	Thr	Gly	His	Leu	Lys	Cys	Arg	Leu	Arg	
		465					470					475				
atg	gac	aag	cta	cag	ctc	aaa	gga	atg	tca	tac	tct	atg	tgc	aca	gga	2391
Met	Asp	Lys	Leu	Gln	Leu	Lys	Gly	Met	Ser	Tyr	Ser	Met	Cys	Thr	Gly	
	480					485					490					

															811252	
aag	ttt	aaa	gtt	gtg	aag	gaa	ata	gca	gaa	aca	caa	cat	gga	aca	ata	2439
Lys	Phe	Lys	Val	Val	Lys	Glu	Ile	Ala	Glu	Thr	Gln	His	Gly	Thr	Ile	
495					500					505					510	
ggt	atc	aga	gtg	caa	tat	gaa	ggg	gac	ggc	tct	cca	tgc	aag	atc	cct	2487
Val	Ile	Arg	Val	Gln	Tyr	Glu	Gly	Asp	Gly	Ser	Pro	Cys	Lys	Ile	Pro	
				515					520					525		
ttt	gag	ata	atg	gat	ttg	gaa	aaa	aga	cat	gtc	tta	ggt	cgc	ctg	att	2535
Phe	Glu	Ile	Met	Asp	Leu	Glu	Lys	Arg	His	Val	Leu	Gly	Arg	Leu	Ile	
			530					535					540			
aca	gtc	aac	cca	att	gtg	aca	gaa	aaa	gat	agc	cca	gtc	aac	ata	gaa	2583
Thr	Val	Asn	Pro	Ile	Val	Thr	Glu	Lys	Asp	Ser	Pro	Val	Asn	Ile	Glu	
		545					550					555				
gca	gaa	cct	cca	ttc	gga	gac	agc	cac	atc	atc	ata	gga	gta	gag	ccg	2631
Ala	Glu	Pro	Pro	Phe	Gly	Asp	Ser	His	Ile	Ile	Ile	Gly	Val	Glu	Pro	
	560					565					570					
gga	caa	ctg	aag	ctc	aac	tgg	ttt	aag	aaa	gga	agt	tct	atc	ggc	caa	2679
Gly	Gln	Leu	Lys	Leu	Asn	Trp	Phe	Lys	Lys	Gly	Ser	Ser	Ile	Gly	Gln	
575					580					585					590	
atg	ttt	gag	aca	aca	atg	agg	ggg	gcg	aag	aga	atg	gcc	att	tta	ggt	2727
Met	Phe	Glu	Thr	Thr	Met	Arg	Gly	Ala	Lys	Arg	Met	Ala	Ile	Leu	Gly	
				595					600					605		
gac	aca	gcc	tgg	gat	ttt	gga	tcc	ttg	gga	gga	gtg	ttt	aca	tct	ata	2775
Asp	Thr	Ala	Trp	Asp	Phe	Gly	Ser	Leu	Gly	Gly	Val	Phe	Thr	Ser	Ile	
			610					615					620			
gga	aag	gct	ctc	cac	caa	gtg	ttt	ggt	ggt	gcc	ttc	aga	aca	ctc	ttt	2823
Gly	Lys	Ala	Leu	His	Gln	Val	Phe	Gly	Gly	Ala	Phe	Arg	Thr	Leu	Phe	
		625					630					635				
ggg	gga	atg	tct	tgg	atc	aca	caa	ggg	cta	atg	ggt	gcc	cta	ctg	ctc	2871
Gly	Gly	Met	Ser	Trp	Ile	Thr	Gln	Gly	Leu	Met	Gly	Ala	Leu	Leu	Leu	
	640					645					650					
tgg	atg	ggc	gtc	aac	gca	cga	gac	cga	tca	att	gct	ttg	gcc	ttc	tta	2919
Trp	Met	Gly	Val	Asn	Ala	Arg	Asp	Arg	Ser	Ile	Ala	Leu	Ala	Phe	Leu	
655					660					665					670	
gcc	aca	ggg	ggt	gtg	ctc	gtg	ttc	tta	gcg	acc	aat	gtg	cat	gct		2964
Ala	Thr	Gly	Gly	Val	Leu	Val	Phe	Leu	Ala	Thr	Asn	Val	His	Ala		
				675					680					685		
taattagttt gggcgggccgc tcgagcatgc atctagaggg ccctattcta tagtgtcacc																3024
taaagctag agctcgctga tcagcctcga ctgtgccttc tagttgccag ccatctgttg																3084
tttggccctc ccccgctgcct tccttgaccc tgggaaggtgc cactcccact gtcctttcct																3144
aataaaaatga ggaaattgca tcgcattgtc tgagtaggtg tcattctatt ctgggggggtg																3204
gggtggggca ggacagcaag ggggaggatt gggaagacaa tagcaggcat gctggggatg																3264
cggtgggctc tatggcttct gaggcgaaaa gaaccagctg cattaatgaa tcggccaacg																3324
cgcggggaga ggcggtttgc gtattgggcg ctcttcgcgt tcctcgctca ctgactcgct																3384
gcgctcggtc gttcggctgc ggcgagcgg atcagctcac tcaaaggcgg taatacggtt																3444

811252

atccacagaa	tcaggggata	acgcaggaaa	gaacatgtga	gcaaaaggcc	agcaaaaggc	3504
caggaaccgt	aaaaaggccg	cgttgctggc	gtttttccat	aggctccgcc	cccctgacga	3564
gcatcacaaa	aatcgacgct	caagtcagag	gtggcgaaac	ccgacaggac	tataaagata	3624
ccaggcgttt	ccccctggaa	gctccctcgt	gcgctctcct	gttccgaccc	tgccgcttac	3684
cggataacctg	tccgcctttc	tcccttcggg	aagcgtggcg	ctttctcata	gctcacgctg	3744
taggtatctc	agttcgggtg	aggtcgttcg	ctccaagctg	ggctgtgtgc	acgaaccccc	3804
cgttcagccc	gaccgctgcg	ccttatccgg	taactatcgt	cttgagtcca	acccggtaag	3864
acacgactta	tcgccactgg	cagcagccac	tggtaacagg	attagcagag	cgaggtatgt	3924
aggcggtgct	acagagttct	tgaagtggcg	gcctaactac	ggctacacta	gaagaacagt	3984
at ttgggtatc	tcgctctcgc	tgaagccagt	taccttcgga	aaaagagttg	gtagctcttg	4044
atccggcaaa	caaaccaccg	ctggtagcgg	tggttttttt	gtttgcaagc	agcagattac	4104
gcgcagaaaa	aaaggatctc	aagaagatcc	tttgatcttt	tctacggggt	ctgacgctca	4164
gtggaacgaa	aactcacgtt	aagggttttt	ggcatgaga	ttatcaaaaa	ggatcttcac	4224
ctagatcctt	ttaaattaaa	aatgaagttt	taaatcaatc	taaagtatat	atgagtaaac	4284
ttggcttgac	agttaccaat	gcttaatcag	tgaggcacct	atctcagcga	tctgtctatt	4344
tcgttcatcc	atagttgcct	gactccccgt	cgtgtagata	actacgatac	gggagggcct	4404
accatctggc	cccagtgtcg	caatgatacc	gcgagaccca	cgctcaccgg	ctccagattt	4464
atcagcaata	aaccagccag	ccggaagggc	cgagcgcaga	agtggtcctg	caactttatc	4524
cgctcccatc	cagtctatta	attgttgccg	ggaagctaga	gtaagtagtt	cgccagttaa	4584
tagtttgccg	aacgttggtg	ccattgctac	aggcatcgtg	gtgtcacgct	cgtcgtttgg	4644
tatggcttca	ttcagctccg	gttcccaacg	atcaaggcga	gttacatgat	cccccatggt	4704
gtgcaaaaaa	gcggttagct	ccttcgggtc	tccgatcgtt	gtcagaagta	agttggccgc	4764
agtgttatca	ctcatgggta	tggcagcact	gcataattct	cttactgtca	tgccatccgt	4824
aagatgcttt	tctgtgactg	gtgagtactc	aaccaagtca	ttctgagaat	agtgtatgcg	4884
gcgaccgagt	tgctcttgcc	cggcgtcaat	acgggataat	accgcgccac	atagcagaac	4944
tttaaaagtg	ctcatcattg	gaaaacgttc	ttcggggcga	aaactctcaa	ggatcttacc	5004
gctgttgaga	tccagttcga	tgtaaccac	tcgtgcaccc	aactgatctt	cagcatcttt	5064
tactttcacc	agcgtttctg	ggtgagcaaa	aacaggaagg	caaaatgccg	caaaaaagg	5124
aataagggcg	acacggaaat	gttgaatact	catactcttc	ctttttcaat	attattgaag	5184
catttatcag	ggttattgtc	tcagtagcgg	atacatattt	gaatgtattt	agaaaaataa	5244
acaaataggg	gttccgcgca	catttccccg	aaaagtgcc	cctgacgtc		5293

811252

<210> 45
<211> 685
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct
<400> 45

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15
Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly
20 25 30
Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
35 40 45
Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
50 55 60
Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
65 70 75 80
Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
85 90 95
Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg
100 105 110
Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu
115 120 125
Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val
130 135 140
Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met
145 150 155 160
Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala
165 170 175
Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg
180 185 190
Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly
195 200 205

811252

Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met
210 215 220

Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala
225 230 235 240

Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr
245 250 255

Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu
260 265 270

Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp
275 280 285

Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val
290 295 300

Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val
305 310 315 320

Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly
325 330 335

Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile
340 345 350

Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr
355 360 365

Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn
370 375 380

Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg
385 390 395 400

Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr
405 410 415

Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn
420 425 430

Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly
435 440 445

Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser
450 455 460

811252

Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp
465 470 475 480

Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe
485 490 495

Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile
500 505 510

Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu
515 520 525

Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val
530 535 540

Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu
545 550 555 560

Pro Pro Phe Gly Asp Ser His Ile Ile Ile Gly Val Glu Pro Gly Gln
565 570 575

Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln Met Phe
580 585 590

Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly Asp Thr
595 600 605

Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile Gly Lys
610 615 620

Ala Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
625 630 635 640

Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
645 650 655

Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
660 665 670

Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
675 680 685

<210> 46
<211> 5293
<212> DNA
<213> Artificial Sequence

<220>

811252

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> CDS

<222> (910)..(2964)

<400> 46

```

gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg      60
ccgcatagtt aagccagtat ctgctcccctg cttgtgtgtt ggaggtcgct gagtagtgcg      120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180
ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240
gattattgac tagttattaa tagtaatcaa ttacgggggtc attagttcat agcccatata      300
tggagttccg cgttacataa cttacggtaa atggcccgcg tggctgaccg cccaacgacc      360
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420
attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt      480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt      540
atgccagta catgacctta tgggactttc ctacttgga gtacatctac gtattagtca      600
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg      660
actcacgggg atttccaagt ctccaccca ttgacgtcaa tgggagtttg ttttggcacc      720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc ccattgacg caaatgggcg      780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaacca      840
ctgcttactg gcttatcgaa attaatacga ctactatag ggagaccaa gcttggtacc      900
gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc      951
      Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
      1          5          10

ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt      999
Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg
15          20          25          30

aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt      1047
Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser
35          40          45

ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc      1095
Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala
50          55          60

atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc      1143
Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro
65          70          75

ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct      1191
Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser
80          85          90

acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat      1239

```

															811252	
Thr	Ser	Thr	Trp	Val	Thr	Tyr	Gly	Thr	Cys	Thr	Thr	Met	Gly	Glu	His	
95					100					105					110	
aga	aga	gaa	aaa	aga	tca	gtg	gca	ctc	ggt	cca	cat	gtg	gga	atg	gga	1287
Arg	Arg	Glu	Lys	Arg	Ser	Val	Ala	Leu	Val	Pro	His	Val	Gly	Met	Gly	
				115					120					125		
ctg	gag	aca	cga	act	gaa	aca	tgg	atg	tca	tca	gaa	ggg	gcc	tgg	aaa	1335
Leu	Glu	Thr	Arg	Thr	Glu	Thr	Trp	Met	Ser	Ser	Glu	Gly	Ala	Trp	Lys	
			130					135					140			
cat	gtc	cag	aga	att	gaa	act	tgg	atc	ttg	aga	cat	cca	ggc	ttc	acc	1383
His	Val	Gln	Arg	Ile	Glu	Thr	Trp	Ile	Leu	Arg	His	Pro	Gly	Phe	Thr	
		145					150					155				
atg	atg	gca	gca	atc	ctg	gca	tac	acc	ata	gga	acg	aca	cat	ttc	caa	1431
Met	Met	Ala	Ala	Ile	Leu	Ala	Tyr	Thr	Ile	Gly	Thr	Thr	His	Phe	Gln	
	160					165					170					
aga	gcc	ctg	att	ttc	atc	tta	ctg	aca	gct	gtc	act	cct	tca	atg	aca	1479
Arg	Ala	Leu	Ile	Phe	Ile	Leu	Leu	Thr	Ala	Val	Thr	Pro	Ser	Met	Thr	
175					180					185					190	
atg	cgt	tgc	ata	gga	atg	tca	aat	aga	gac	ttt	gtg	gaa	ggg	gtt	tca	1527
Met	Arg	Cys	Ile	Gly	Met	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Val	Ser	
			195						200					205		
gga	gga	agc	tgg	gtt	gac	ata	gtc	tta	gaa	cat	ggg	agc	tgt	gtg	acg	1575
Gly	Gly	Ser	Trp	Val	Asp	Ile	Val	Leu	Glu	His	Gly	Ser	Cys	Val	Thr	
			210					215					220			
acg	atg	gca	aaa	aac	aaa	cca	aca	ttg	gat	ttt	gaa	ctg	ata	aaa	aca	1623
Thr	Met	Ala	Lys	Asn	Lys	Pro	Thr	Leu	Asp	Phe	Glu	Leu	Ile	Lys	Thr	
		225					230					235				
gaa	gcc	aaa	cag	cct	gcc	acc	cta	agg	aag	tac	tgt	ata	gag	gca	aag	1671
Glu	Ala	Lys	Gln	Pro	Ala	Thr	Leu	Arg	Lys	Tyr	Cys	Ile	Glu	Ala	Lys	
	240				245						250					
cta	acc	aac	aca	aca	aca	gaa	tct	cgc	tgc	cca	aca	caa	ggg	gaa	ccc	1719
Leu	Thr	Asn	Thr	Thr	Thr	Glu	Ser	Arg	Cys	Pro	Thr	Gln	Gly	Glu	Pro	
255					260				265						270	
agc	cta	aat	gaa	gag	cag	gac	aaa	agg	ttc	gtc	tgc	aaa	cac	tcc	atg	1767
Ser	Leu	Asn	Glu	Glu	Gln	Asp	Lys	Arg	Phe	Val	Cys	Lys	His	Ser	Met	
			275						280					285		
gta	gac	aga	gga	tgg	gga	aat	gga	tgt	gga	cta	ttt	gga	aag	gga	ggc	1815
Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Gly	
			290					295					300			
att	gtg	acc	tgt	gct	atg	ttc	aga	tgc	aaa	aag	aac	atg	gaa	gga	aaa	1863
Ile	Val	Thr	Cys	Ala	Met	Phe	Arg	Cys	Lys	Lys	Asn	Met	Glu	Gly	Lys	
		305					310					315				
gtt	gtg	caa	cca	gaa	aac	ttg	gaa	tac	acc	att	gtg	ata	aca	cct	cac	1911
Val	Val	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Thr	Ile	Val	Ile	Thr	Pro	His	
	320					325					330					
tca	ggg	gaa	gag	cat	gca	gtc	gga	aat	gac	aca	gga	aaa	cat	ggc	aag	1959
Ser	Gly	Glu	Glu	His	Ala	Val	Gly	Asn	Asp	Thr	Gly	Lys	His	Gly	Lys	
335					340					345					350	

															811252	
gaa	atc	aaa	ata	aca	cca	cag	agt	tcc	atc	aca	gaa	gca	gaa	ttg	aca	2007
Glu	Ile	Lys	Ile	Thr	Pro	Gln	Ser	Ser	Ile	Thr	Glu	Ala	Glu	Leu	Thr	
				355					360					365		
ggt	tat	ggc	act	gtc	aca	atg	gag	tgc	tct	cca	aga	acg	ggc	ctc	gac	2055
Gly	Tyr	Gly	Thr	Val	Thr	Met	Glu	Cys	Ser	Pro	Arg	Thr	Gly	Leu	Asp	
				370					375					380		
ttc	aat	gag	atg	gtg	ttg	ttg	cag	atg	gaa	aat	aaa	gct	tgg	ctg	gtg	2103
Phe	Asn	Glu	Met	Val	Leu	Leu	Gln	Met	Glu	Asn	Lys	Ala	Trp	Leu	Val	
		385					390					395				
cac	agg	caa	tgg	ttc	cta	gac	ctg	ccg	tta	cca	tgg	ttg	ccc	gga	gcg	2151
His	Arg	Gln	Trp	Phe	Leu	Asp	Leu	Pro	Leu	Pro	Trp	Leu	Pro	Gly	Ala	
		400					405					410				
gac	aca	caa	ggg	tca	aat	tgg	ata	cag	aaa	gag	aca	ttg	gtc	act	ttc	2199
Asp	Thr	Gln	Gly	Ser	Asn	Trp	Ile	Gln	Lys	Glu	Thr	Leu	Val	Thr	Phe	
		415					420					425				
aaa	aat	ccc	cat	gcg	aag	aaa	cag	gat	ggt	ggt	ggt	tta	gga	tcc	caa	2247
Lys	Asn	Pro	His	Ala	Lys	Lys	Gln	Asp	Val	Val	Val	Leu	Gly	Ser	Gln	
				435					440					445		
gaa	ggg	gcc	atg	cac	aca	gca	ctt	aca	ggg	gcc	aca	gaa	atc	caa	atg	2295
Glu	Gly	Ala	Met	His	Thr	Ala	Leu	Thr	Gly	Ala	Thr	Glu	Ile	Gln	Met	
				450					455					460		
tca	tca	gga	aac	tta	ctc	ttc	aca	gga	cat	ctc	aag	tgc	agg	ctg	aga	2343
Ser	Ser	Gly	Asn	Leu	Leu	Phe	Thr	Gly	His	Leu	Lys	Cys	Arg	Leu	Arg	
		465					470					475				
atg	gac	aag	cta	cag	ctc	aaa	gga	atg	tca	tac	tct	atg	tgc	aca	gga	2391
Met	Asp	Lys	Leu	Gln	Leu	Lys	Gly	Met	Ser	Tyr	Ser	Met	Cys	Thr	Gly	
		480					485					490				
aag	ttt	aaa	gtt	gtg	aag	gaa	ata	gca	gaa	aca	caa	cat	gga	aca	ata	2439
Lys	Phe	Lys	Val	Val	Lys	Glu	Ile	Ala	Glu	Thr	Gln	His	Gly	Thr	Ile	
		495					500					505				
gtt	atc	aga	gtg	caa	tat	gaa	ggg	gac	ggc	tct	cca	tgc	aag	atc	cct	2487
Val	Ile	Arg	Val	Gln	Tyr	Glu	Gly	Asp	Gly	Ser	Pro	Cys	Lys	Ile	Pro	
				515					520					525		
ttt	gag	ata	atg	gat	ttg	gaa	aaa	aga	cat	gtc	tta	ggt	cgc	ctg	att	2535
Phe	Glu	Ile	Met	Asp	Leu	Glu	Lys	Arg	His	Val	Leu	Gly	Arg	Leu	Ile	
				530					535					540		
aca	gtc	aac	cca	att	gtg	aca	gaa	aaa	gat	agc	cca	gtc	aac	ata	gaa	2583
Thr	Val	Asn	Pro	Ile	Val	Thr	Glu	Lys	Asp	Ser	Pro	Val	Asn	Ile	Glu	
		545					550					555				
gca	gaa	cct	cca	ttc	gga	gac	agc	tac	atc	atc	ata	gga	gta	gag	ccg	2631
Ala	Glu	Pro	Pro	Phe	Gly	Asp	Ser	Tyr	Ile	Ile	Ile	Gly	Val	Glu	Pro	
		560					565					570				
gga	caa	ctg	aag	ctc	aac	tgg	ttt	aag	aaa	gga	agc	acg	ctg	ggc	aag	2679
Gly	Gln	Leu	Lys	Leu	Asn	Trp	Phe	Lys	Lys	Gly	Ser	Thr	Leu	Gly	Lys	
		575					580					585				
gcc	ttt	tca	aca	act	ttg	aag	gga	gct	caa	aga	ctg	gca	gcg	ttg	ggc	2727
Ala	Phe	Ser	Thr	Thr	Leu	Lys	Gly	Ala	Gln	Arg	Leu	Ala	Ala	Leu	Gly	
				595					600					605		

811252

gac aca gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile 610 615 620	2775
gga aaa gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe 625 630 635	2823
ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu 640 645 650	2871
tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu 655 660 665 670	2919
gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala 675 680 685	2964
taattagttt gagcggccgc tcgagcatgc atctagaggg ccctattcta tagtgtcacc	3024
taaatgctag agctcgctga tcagcctcga ctgtgccttc tagttgccag ccattctgtt	3084
tttgcccctc ccccgtgcct tccttgaccc tggaaggtgc cactcccact gtcctttcct	3144
aataaaatga ggaaattgca tcgcattgtc tgagtaggtg tcattctatt ctgggggggtg	3204
gggtggggca ggacagcaag ggggaggatt gggaagacaa tagcaggcat gctgggggatg	3264
cggtgggctc tatggcttct gaggcggaaa gaaccagctg cattaatgaa tcggccaacg	3324
cgcggggaga ggcggtttgc gtattgggcg ctcttcgcgt tcctcgctca ctgactcgct	3384
gcgctcggtc gttcggctgc ggcgagcgg atcagctcac tcaaaggcgg taatacgggt	3444
atccacagaa tcaggggata acgcaggaaa gaacatgtga gcaaaaggcc agcaaaaggc	3504
caggaaccgt aaaaaggccg cgttgctggc gtttttccat aggctccgcc cccctgacga	3564
gcatcacaaa aatcgacgct caagtcagag gtggcgaaac ccgacaggac tataaagata	3624
ccaggcgttt ccccttgaa gtccttcgt gcgctctcct gttccgacct tgccgcttac	3684
cggatacctg tccgcctttc tcccttcggg aagcgtggcg ctttctcaat gctcacgctg	3744
taggtatctc agttcggtgt aggtcgttcg ctccaagctg ggctgtgtgc acgaaccccc	3804
cgttcagccc gaccgctgcg cttatccgg taactatcgt cttgagtcca acccggttaag	3864
acacgactta tcgccactgg cagcagccac tggtaacagg attagcagag cgaggatatgt	3924
aggcgggtgct acagagttct tgaagtgggt gcctaactac ggctacacta gaaggacagt	3984
atttggtatc tgcgctctgc tgaagccagt taccttcgga aaaagagttg gtagctcttg	4044
atccggcaaaa caaaccaccg ctggtagcgg tgggtttttt gtttgcaagc agcagattac	4104
gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt tctacggggt ctgacgctca	4164
gtggaacgaa aactcacgtt aagggaattt ggtcatgaga ttatcaaaaa ggatcttcac	4224

811252

ctagatcctt ttaaattaaa aatgaagttt taaatcaatc taaagtatat atgagtaaac 4284
 ttggtctgac agttaccaat gcttaatcag tgaggcacct atctcagcga tctgtctatt 4344
 tcgttcatcc atagttgcct gactccccgt cgtgtagata actacgatac gggagggcctt 4404
 accatctggc cccagtgcctg caatgatacc gcgagaccca cgctcaccgg ctccagattt 4464
 atcagcaata aaccagccag ccggaagggc cgagcgcaga agtggtcctg caactttatc 4524
 cgcctccatc cagtctatta attgttgccg ggaagctaga gtaagtagtt cgccagttaa 4584
 tagtttgccg aacgttggtg ccattgctac aggcacgtg gtgtcacgct cgtcgtttgg 4644
 tatggcttca ttcagctccg gttcccaacg atcaaggcga gttacatgat ccccatgtt 4704
 gtgcaaaaaa gcggttagct ccttcggtcc tccgatcgtt gtcagaagta agttggccgc 4764
 agtgttatca ctcatggtta tggcagcact gcataattct cttactgtca tgccatccgt 4824
 aagatgcttt tctgtgactg gtgagtactc aaccaagtca ttctgagaat agtgtatgcg 4884
 gcgaccgagt tgctcttgcc cggcgtcaat acgggataat accgcgccac atagcagaac 4944
 tttaaaagtg ctcatcattg gaaaacgttc ttcggggcga aaactctcaa ggatcttacc 5004
 gctgttgaga tccagttcga tgtaaccac tcgtgcaccc aactgatctt cagcatcttt 5064
 tactttcacc agcgtttctg ggtgagcaaa aacaggaagg caaaatgccg caaaaaaggg 5124
 aataagggcg acacggaaat gttgaatact catactcttc ctttttcaat attattgaag 5184
 catttatcag gggtattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa 5244
 acaaataggg gttccgcgca ctttccccg aaaagtgcc cctgacgct 5293

<210> 47
 <211> 685
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 47

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
 1 5 10 15

Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly
 20 25 30

Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
 35 40 45

Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
 50 55 60

811252

Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
65 70 75 80

Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
85 90 95

Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg
100 105 110

Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu
115 120 125

Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val
130 135 140

Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met
145 150 155 160

Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala
165 170 175

Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg
180 185 190

Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly
195 200 205

Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met
210 215 220

Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala
225 230 235 240

Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr
245 250 255

Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu
260 265 270

Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp
275 280 285

Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val
290 295 300

Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val
305 310 315 320

811252

Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly
325 330 335

Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile
340 345 350

Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr
355 360 365

Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn
370 375 380

Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg
385 390 395 400

Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr
405 410 415

Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn
420 425 430

Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly
435 440 445

Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser
450 455 460

Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp
465 470 475 480

Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe
485 490 495

Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile
500 505 510

Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu
515 520 525

Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val
530 535 540

Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu
545 550 555 560

Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro Gly Gln
565 570 575

811252

Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys Ala Phe
580 585 590

Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr
595 600 605

Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys
610 615 620

Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
625 630 635 640

Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
645 650 655

Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
660 665 670

Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
675 680 685

<210> 48
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 48
tgtgcaggcg ccttccattt aaccacacgt aacg 34

<210> 49
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 49
tcgagcggcc gctcaactaa ttaggcctgc accatgactc 40

<210> 50
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 50

cttatcgaaa ttaatacgac tcactatagg 30

<210> 51
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct

<400> 51
 atagattgct ccaaacactt ggtgg 25

<210> 52
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct

<400> 52
 actccatagg aaaagccgtt cacc 24

<210> 53
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct

<400> 53
 gcgagctcta gcatttaggt gacactatag 30

<210> 54
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct

<400> 54
 ctccaccaag tgtttggtgg tgccttcaga aca 33

<210> 55
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct

<400> 55

Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr
 1 5 10

<210> 56
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 56
 cttatcga aa ttaatacgac tcactatagg 30

 <210> 57
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 57
 gaattcgct cacttccttt cttaaaccag ttgagcttc 39

 <210> 58
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 58
 ggaattcgtc tcggaagcac gctgggcaag g 31

 <210> 59
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 59
 gcgagctcta gcatttaggt gacactatag 30

 <210> 60
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 60
 aactggttta agaaaggaag cacgctgggc gcc 33

 <210> 61

811252

<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 61

Asn Trp Lys Lys Gly Ser Thr Leu Gly Lys Ala
1 5 10

<210> 62
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 62

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Cys Ala Gly Ala Met Lys Leu Ser Asn Phe Gln Gly
20 25 30

Lys

<210> 63
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 63

Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met
1 5 10 15

Trp Leu Ala Ser Leu Ala Val Val Ile Ala Gly Thr Ser Ala Met Lys
20 25 30

Leu Ser Asn Phe Gln Gly Lys
35

<210> 64
<211> 33
<212> PRT
<213> Artificial Sequence

<220>

811252

<223> Synthetic construct

<400> 64

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala Met Lys Leu Ser Asn Phe Gln Gly
20 25 30

Lys